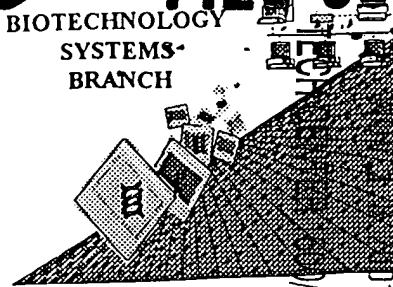


RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

FILE COPY

RECEIVED



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/039177D

Source:

AU 1647

Date Processed by STIC:

10/18/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1647

RAW SEQUENCE LISTING

DATE: 10/15/2001

PATENT APPLICATION: US/09/039,177D

TIME: 13:47:03

Input Set : A:\Lud-5539 sequence listing.txt

Output Set: N:\CRF3\10152001\I039177D.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Kohei MIYAZONO; Takeshe IMAMURA; Peter DEN DIJKE
7 (ii) TITLE OF INVENTION: ISOLATED ALK-1 PROTEIN, NUCLEIC ACIDS ENCODING
8 IT, AND USES THEREOF

10 (iii) NUMBER OF SEQUENCES: 46

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
14 (B) STREET: 801 Pennsylvania Avenue, N.W.
15 (C) CITY: Washington
16 (D) STATE: District of Columbia
17 (E) COUNTRY: USA
18 (F) ZIP: 20004

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
22 (B) COMPUTER: IBM PS/2
23 (C) OPERATING SYSTEM: PC-DOS
24 (D) SOFTWARE: Wordperfect

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/09/039,177D
C--> 28 (B) FILING DATE: 13-Mar-1998
29 (C) CLASSIFICATION: 435

59 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: PCT/GB93/02367
33 (B) FILING DATE: November 17, 1993
36 (A) APPLICATION NUMBER: GB 9224057.1
37 (B) FILING DATE: November 17, 1992
40 (A) APPLICATION NUMBER: GB 9304677.9
41 (B) FILING DATE: March 8, 1993
44 (A) APPLICATION NUMBER: GB 9304680.3
45 (B) FILING DATE: March 8, 1993
48 (A) APPLICATION NUMBER: 9311047.6
49 (B) FILING DATE: May 28, 1993
52 (A) APPLICATION NUMBER: 9313763.6
53 (B) FILING DATE: July 2, 1993
56 (A) APPLICATION NUMBER: 9136099.2
57 (B) FILING DATE: August 3, 1993
60 (A) APPLICATION NUMBER: 321344.5
61 (B) FILING DATE: October 15, 1993

63 (viii) ATTORNEY/AGENT INFORMATION:

64 (A) NAME: Mary Anne Schofield
65 (B) REGISTRATION NUMBER: 36,669
66 (C) REFERENCE/DOCKET NUMBER: LUD 5539 CIP - JEL/MAS

68 (ix) TELECOMMUNICATION INFORMATION:

69 (A) TELEPHONE: (202) 662-0200
70 (B) TELEFAX: (202) 662-4643

Does Not Comply
Corrected Diskette Needed

See page 2, 4, 5, 6
and 7

RAW SEQUENCE LISTING

DATE: 10/15/2001

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TIME: 13:47:03

Input Set : A:\Lud-5539 sequence listing.txt

Output Set: N:\CRF3\10152001\I039177D.raw

ERRORED SEQUENCES

74 (2) INFORMATION FOR SEQ ID NO: 1:
 75 (i) SEQUENCE CHARACTERISTICS:
 76 (A) LENGTH: 1984 base pairs
 77 (B) TYPE: nucleic acid
 78 (C) STRANDEDNESS: unknown
 79 (D) TOPOLOGY: linear
 81 (ii) MOLECULE TYPE: cDNA
 83 (iii) HYPOTHETICAL: NO
 C--> 85 (iv) ANTI-SENSE: NO
 87 (v) FRAGMENT TYPE: internal
 89 (vi) ORIGINAL SOURCE:
 90 (A) ORGANISM: Homo sapiens
 92 (ix) FEATURE:
 93 (A) NAME/KEY: CDS
 94 (B) LOCATION: 283..1791
 96 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 E--> 98 AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA
 99 CGCTGGAATA 60
 E--> 101 AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC
 102 CAGCTGCGCC 120
 E--> 104 GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC
 105 AGCCCGCCGT 180
 E--> 107 CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC
 108 GGTCCGCCGA 240
 E--> 110 AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC
 W--> 111 294
 112 Met Thr Leu Gly
 113 1
 114 TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG 342
 115 Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln
 116 5 10 15 20
 118 GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT 390
 119 Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys
 120 25 30 35
 122 GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA 438
 123 Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr
 124 40 45 50
 126 GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC 486
 127 Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly
 128 55 60 65
 130 TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC 534
 131 Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe
 132 70 75 80
 134 GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC 582
 135 Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser
 136 85 90 95 100
 138 CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT 630
 139 Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp

Does Not Comply
 Corrected Diskette Needed

69 Errored

RAW SEQUENCE LISTING

DATE: 10/15/2001

PATENT APPLICATION: US/09/039,177D

TIME: 13:47:03

Input Set : A:\Lud-5539 sequence listing.txt

Output Set: N:\CRF3\10152001\I039177D.raw

140		105		110		115		
142	GGC CAG CTG	GCC CTG ATC CTG	GGC CCC GTG CTG	GCC TTG CTG	GCC CTG			678
143	Gly Gln Leu	Ala Leu Ile Leu	Gly Pro Val Leu	Ala Leu Ala Leu				
144		120		125		130		
146	GTG GCC CTG	GGT GTC CTG	GGC CTG TGG	CAT GTC CGA	CGG AGG CAG	GAG		726
147	Val Ala Leu	Gly Val Leu	Gly Leu Trp	His Val Arg	Arg Arg Gln	Glu		
148		135		140		145		
150	AAG CAG CGT	GGC CTG CAC	AGC GAG CTG	GGA GAG TCC	AGT CTC ATC	CTG		774
151	Lys Gln Arg	Gly Leu His	Ser Glu Leu	Gly Glu Ser	Ser Leu Ile	Leu		
152		150		155		160		
154	AAA GCA TCT	GAG CAG GGC	GAC ACG ATG	TTG GGG GAC	CTC CTG GAC	AGT		822
155	Lys Ala Ser	Glu Gln Gly	Asp Thr Met	Leu Gly Asp	Leu Leu Asp	Ser		
156	165		170		175		180	
158	GAC TGC ACC	ACA GGG AGT	GGC TCA GGG	CTC CCC TTC	CTG GTG CAG	AGG		870
159	Asp Cys Thr	Thr Gly Ser	Gly Ser Gly	Leu Pro Phe	Leu Val Gln	Arg		
160		185		190		195		
162	ACA GTG GCA	CGG CAG GTT	GCC TTG GTG	GAG TGT GTG	GGA AAA GGC	CGC		918
163	Thr Val Ala	Arg Gln Val	Ala Leu Val	Glu Cys Val	Gly Lys Gly	Arg		
164		200		205		210		
166	TAT GGC GAA	GTG TGG CGG	GGC TTG TGG	CAC GGT GAG	AGT GTG GCC	GTC		966
167	Tyr Gly Glu	Val Trp Arg	Gly Leu Trp	His Gly Glu	Ser Val Ala	Val		
168		215		220		225		
170	AAG ATC TTC	TCC TCG AGG	GAT GAA CAG	TCC TGG TTC	CGG GAG ACT	GAG		1014
171	Lys Ile Phe	Ser Ser Arg	Asp Glu Gln	Ser Trp Phe	Arg Glu Thr	Glu		
172		230		235		240		
174	ATC TAT AAC	ACA GTA TTG	CTC AGA CAC	GAC AAC ATC	CTA GGC TTC	ATC		1062
175	Ile Tyr Asn	Thr Val Leu	Leu Arg His	Asp Asn Ile	Leu Gly Phe	Ile		
176	245		250		255		260	
178	GCC TCA GAC	ATG ACC TCC	CGC AAC TCG	AGC ACG CAG	CTG TGG CTC	ATC		1110
179	Ala Ser Asp	Met Thr Ser	Arg Asn Ser	Ser Thr Gln	Leu Trp Leu	Ile		
180		265		270		275		
182	ACG CAC TAC	CAC GAG CAC	GGC TCC CTC	TAC GAC TTT	CTG CAG AGA	CAG		1158
183	Thr His Tyr	His Glu His	Gly Ser Leu	Tyr Asp Phe	Leu Gln Arg	Gln		
184		280		285		290		
186	ACG CTG GAG	CCC CAT CTG	GCT CTG AGG	CTA GCT GTG	TCC GCG GCA	TGC		1206
187	Thr Leu Glu	Pro His Leu	Ala Leu Arg	Leu Ala Val	Ser Ala Ala	Cys		
188		295		300		305		
190	GGC CTG GCG	CAC CTG CAC	GTG GAG ATC	TTC GGT ACA	CAG GGC AAA	CCA		1254
191	Gly Leu Ala	His Leu His	Val Glu Ile	Phe Gly Thr	Gln Gly Lys	Pro		
192		310		315		320		
194	GCC ATT GCC	CAC CGC GAC	TTC AAG AGC	CGC AAT GTG	CTG GTC AAG	AGC		1302
195	Ala Ile Ala	His Arg Asp	Phe Lys Ser	Arg Asn Val	Leu Val Lys	Ser		
196	325		330		335		340	
198	AAC CTG CAG	TGT TGC ATC	GCC GAC CTG	GGC CTG GCT	GTG ATG CAC	TCA		1350
199	Asn Leu Gln	Cys Cys Ile	Ala Asp Leu	Gly Leu Ala	Val Met His	Ser		
200		345		350		355		
202	CAG GGC AGC	GAT TAC CTG	GAC ATC GGC	AAC AAC CCG	AGA GTG GGC	ACC		1398
203	Gln Gly Ser	Asp Tyr Leu	Asp Ile Gly	Asn Asn Pro	Arg Val Gly	Thr		
204		360		365		370		

RAW SEQUENCE LISTING

DATE: 10/15/2001

PATENT APPLICATION: US/09/039,177D

TIME: 13:47:03

Input Set : A:\Lud-5539 sequence listing.txt

Output Set: N:\CRF3\10152001\I039177D.raw

E--> 206 AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG ATC CGC ACG GAC
W--> 207 1446
208 Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp
W--> 209 375 380 385
211 TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG 1494
212 Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val
W--> 213 390 395 400
215 CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC 1542
216 Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp
W--> 217 405 410 415 420
219 TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG 1590
220 Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu
W--> 221 425 430 435
223 GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT 1638
224 Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro
W--> 225 440 445 450
227 AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG 1686
228 Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met
W--> 229 455 460 465
231 CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG 1734
232 Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg
W--> 233 470 475 480
E--> 235 ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA
W--> 236 1782
237 Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys
W--> 238 485 490 495 500
240 GTG ATT CAA TAGCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC 1831
241 Val Ile Gln
E--> 243 TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT
244 GAGTGTGGTG 1891
E--> 246 TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCCACCC
247 AGCCAAAAAT 1951
249 ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA 1984
329 (2) INFORMATION FOR SEQ ID NO: 3:
330 (i) SEQUENCE CHARACTERISTICS:
331 (A) LENGTH: 2724 base pairs
332 (B) TYPE: nucleic acid
333 (C) STRANDEDNESS: unknown
334 (D) TOPOLOGY: linear
336 (ii) MOLECULE TYPE: cDNA
338 (iii) HYPOTHETICAL: NO
C--> 340 (iv) ANTI-SENSE: NO
342 (v) FRAGMENT TYPE: internal
344 (vi) ORIGINAL SOURCE:
345 (A) ORGANISM: Homo sapiens
347 (ix) FEATURE:
348 (A) NAME/KEY: CDS
349 (B) LOCATION: 104..1630
351 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

misaligned end
numbering

should include this field

RAW SEQUENCE LISTING

DATE: 10/15/2001

PATENT APPLICATION: US/09/039,177D

TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt

Output Set: N:\CRF3\10152001\I039177D.raw

E--> 353 CTCCGAGTAC CCCAGTCACC AGAGTGAGAG AAGCTCTGAA CGAGGGCACG
 354 CGGCTTGAAG 60
 E--> 356 GACTGTGCCC AGATGTGACC AAGAGCCTGC ATTAAGTTGT ACA ATG GTA GAT GGA
 W--> 357 115
 358 Met Val Asp Gly
 359 1
 361 GTG ATG ATT CTT CCT GTG CTT ATC ATG ATT GCT CTC CCC TCC CCT AGT 163
 362 Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu Pro Ser Pro Ser
 363 5 10 15 20
 365 ATG GAA GAT GAG AAG CCC AAG GTC AAC CCC AAA CTC TAC ATG TGT GTG 211
 366 Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu Tyr Met Cys Val
 367 25 30 35
 369 TGT GAA GGT CTC TCC TGC GGT AAT GAG GAC CAC TGT GAA GGC CAG CAG 259
 370 Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu Gly Gln Gln
 371 40 45 50
 373 TGC TTT TCC TCA CTG AGC ATC AAC GAT GGC TTC CAC GTC TAC CAG AAA 307
 374 Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His Val Tyr Gln Lys
 375 55 60 65
 377 GGC TGC TTC CAG GTT TAT GAG CAG GGA AAG ATG ACC TGT AAG ACC CCG 355
 378 Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr Cys Lys Thr Pro
 379 70 75 80
 381 CCG TCC CCT GGC CAA GCT GTG GAG TGC TGC CAA GGC GAC TGG TGT AAC 403
 382 Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly Asp Trp Cys Asn
 383 85 90 95 100
 385 AGG AAC ATC ACG GCC CAG CTG CCC ACT AAA GGA AAA TCC TTC CCT GGA 451
 386 Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys Ser Phe Pro Gly
 387 105 110 115
 389 ACA CAG AAT TTC CAC TTG GAG GTT GGC CTC ATT ATT CTC TCT GTA GTG 499
 390 Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile Leu Ser Val Val
 391 120 125 130
 393 TTC GCA GTA TGT CTT TTA GCC TGC CTG CTG GGA GTT GCT CTC CGA AAA 547
 394 Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val Ala Leu Arg Lys
 395 135 140 145
 397 TTT AAA AGG CGC AAC CAA GAA CGC CTC AAT CCC CGA GAC GTG GAG TAT 595
 398 Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg Asp Val Glu Tyr
 399 150 155 160
 401 GGC ACT ATC GAA GGC CTC ATC ACC ACC AAT GTT GGA GAC AGC ACT TTA 643
 402 Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly Asp Ser Thr Leu
 403 165 170 175 180
 405 GCA GAT TTA TTG GAT CAT TCG TGT ACA TCA GGA AGT GGC TCT GGT CTT 691
 406 Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly Ser Gly Leu
 407 185 190 195
 409 CCT TTT CTG GTA CAA AGA ACA GTG GCT CGC CAG ATT ACA CTG TTG GAG 739
 410 Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile Thr Leu Leu Glu
 411 200 205 210
 413 TGT GTC GGC AAA GGC AGG TAT GGT GAG GTG TGG AGG GGC AGC TGG CAA 787
 414 Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp Gln
 415 215 220 225
 417 GGG GAA AAT GTT GCC GTG AAG ATC TTC TCC TCC CGT GAT GAG AAG TCA 835

Wragged
 Nucleotides

RAW SEQUENCE LISTING

DATE: 10/15/2001

PATENT APPLICATION: US/09/039,177D

TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt

Output Set: N:\CRF3\10152001\I039177D.raw

418	Gly	Glu	Asn	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Lys	Ser	
419		230					235					240					
421	TGG	TTC	AGG	GAA	ACG	GAA	TTG	TAC	AAC	ACT	GTG	ATG	CTG	AGG	CAT	GAA	883
422	Trp	Phe	Arg	Glu	Thr	Glu	Leu	Tyr	Asn	Thr	Val	Met	Leu	Arg	His	Glu	
423	245					250					255					260	
425	AAT	ATC	TTA	GGT	TTC	ATT	GCT	TCA	GAC	ATG	ACA	TCA	AGA	CAC	TCC	AGT	931
426	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	His	Ser	Ser	
427				265						270					275		
429	ACC	CAG	CTG	TGG	TTA	ATT	ACA	CAT	TAT	CAT	GAA	ATG	GGA	TCG	TTG	TAC	979
430	Thr	Gln	Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	Met	Gly	Ser	Leu	Tyr	
431			280						285				290				
433	GAC	TAT	CTT	CAG	CTT	ACT	ACT	CTG	GAT	ACA	GTT	AGC	TGC	CTT	CGA	ATA	1027
434	Asp	Tyr	Leu	Gln	Leu	Thr	Thr	Leu	Asp	Thr	Val	Ser	Cys	Leu	Arg	Ile	
435		295						300				305					
437	GTG	CTG	TCC	ATA	GCT	AGT	GGT	CTT	GCA	CAT	TTG	CAC	ATA	GAG	ATA	TTT	1075
438	Val	Leu	Ser	Ile	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Ile	Glu	Ile	Phe	
439	310						315				320						
E--> 441	GGG	ACC	CAA	GGG	AAA	CCA	GCC	ATT	GCC	CAT	CGA	GAT	TTA	AAG	AGC	AAA	
W--> 442	1123																
443	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	
W--> 444	325				330					335					340		
446	AAT	ATT	CTG	GTT	AAG	AAG	AAT	GGA	CAG	TGT	TGC	ATA	GCA	GAT	TTG	GGC	1171
447	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	
W--> 448				345					350					355			
450	CTG	GCA	GTC	ATG	CAT	TCC	CAG	AGC	ACC	AAT	CAG	CTT	GAT	GTG	GGG	AAC	
451	Leu	Ala	Val	Met	His	Ser	Gln	Ser	Thr	Asn	Gln	Leu	Asp	Val	Gly	Asn	
W--> 452			360					365					370				
454	AAT	CCC	CGT	GTG	GGC	ACC	AAG	CGC	TAC	ATG	GCC	CCC	GAA	GTT	CTA	GAT	1267
455	Asn	Pro	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	
W--> 456		375					380					385					
458	GAA	ACC	ATC	CAG	GTG	GAT	TGT	TTC	GAT	TCT	TAT	AAA	AGG	GTC	GAT	ATT	1315
459	Glu	Thr	Ile	Gln	Val	Asp	Cys	Phe	Asp	Ser	Tyr	Lys	Arg	Val	Asp	Ile	
W--> 460		390				395					400						
462	TGG	GCC	TTT	GGA	CTT	GTT	TTG	TGG	GAA	GTG	GCC	AGG	CGG	ATG	GTG	AGC	1363
463	Trp	Ala	Phe	Gly	Leu	Val	Leu	Trp	Glu	Val	Ala	Arg	Arg	Met	Val	Ser	
W--> 464	405				410					415				420			
466	AAT	GGT	ATA	GTG	GAG	GAT	TAC	AAG	CCA	CCG	TTC	TAC	GAT	GTG	GTT	CCC	1411
467	Asn	Gly	Ile	Val	Glu	Asp	Tyr	Lys	Pro	Pro	Phe	Tyr	Asp	Val	Val	Pro	
W--> 468			425					430				435					
470	AAT	GAC	CCA	AGT	TTT	GAA	GAT	ATG	AGG	AAG	GTA	GTC	TGT	GTG	GAT	CAA	1459
471	Asn	Asp	Pro	Ser	Phe	Glu	Asp	Met	Arg	Lys	Val	Val	Cys	Val	Asp	Gln	
W--> 472			440					445				450					
474	CAA	AGG	CCA	AAC	ATA	CCC	AAC	AGA	TGG	TTC	TCA	GAC	CCG	ACA	TTA	ACC	1507
475	Gln	Arg	Pro	Asn	Ile	Pro	Asn	Arg	Trp	Phe	Ser	Asp	Pro	Thr	Leu	Thr	
W--> 476		455					460				465						
478	TCT	CTG	GCC	AAG	CTA	ATG	AAA	GAA	TGC	TGG	TAT	CAA	AAT	CCA	TCC	GCA	1555
479	Ser	Leu	Ala	Lys	Leu	Met	Lys	Glu	Cys	Trp	Tyr	Gln	Asn	Pro	Ser	Ala	
W--> 480		470				475				480							
482	AGA	CTC	ACA	GCA	CTG	CGT	ATC	AAA	AAG	ACT	TTG	ACC	AAA	ATT	GAT	AAT	1603

not aligned
End of string
numbering

not aligned
amino numbering
1219

RAW SEQUENCE LISTING

DATE: 10/15/2001

PATENT APPLICATION: US/09/039,177D

TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt

Output Set: N:\CRF3\10152001\I039177D.raw

```

483 Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys Ile Asp Asn
W--> 484 485          490          495          500          1650
486 TCC CTC GAC AAA TTG AAA ACT GAC TGT TGACATTTTC ATAGTGTCAA
487 Ser Leu Asp Lys Leu Lys Thr Asp Cys
W--> 488          505
E--> 490 GAAGGAAGAT TTGACGTTGT TGTCATTGTC CAGCTGGGAC CTAATGCTGG
491 CCTGACTGGT 1710
E--> 493 TGTCAGAATG GAATCCATCT GTCTCCCTCC CCAAATGGCT GCTTTGACAA
494 GGCAGACGTC 1770
E--> 496 GTACCCAGCC ATGTGTTGGG GAGACATCAA AACCACCCTA ACCTCGCTCG
497 ATGACTGTGA 1830
E--> 499 ACTGGGCATT TCACGAACTG TTCACACTGC AGAGACTAAT GTTGGACAGA
500 CACTGTTGCA 1890
E--> 502 AAGGTAGGGA CTGGAGGAAC ACAGAGAAAT CCTAAAAGAG ATCTGGGCAT
503 TAAGTCAGTG 1950
E--> 505 GCTTTGCATA GCTTTACAAA GTCTCCTAGA CACTCCCCAC GGGAAACTCA
506 AGGAGGTGGT 2010
E--> 508 GAATTTTTTAA TCAGCAATAT TGCCTGTGCT TCTCTTCTTT ATTGCACTAG
509 GAATTCTTTG 2070
E--> 511 CATTCCCTTAC TTGCACTGTT ACTCTTAATT TTAAAGACCC AACTTGCCAA
512 AATGTTGGCT 2130
E--> 514 GCGTACTCCA CTGGTCTGTC TTTGGATAAT AGGAATTCAA TTTGGCAAAA
515 CAAAATGTAA 2190
E--> 517 TGTCAGACTT TGCTGCATTT TACACATGTG CTGATGTTTA CAATGATGCC
518 GAACATTAGG 2250
E--> 520 AATTGTTTAT ACACAACTTT GCAAATTATT TATTACTTGT GCACTTAGTA
521 GTTTTTACAA 2310
E--> 523 AACTGCTTTG TGCATATGTT AAAGCTTATT TTTATGTGGT CTTATGATTT
524 TATTACAGAA 2370
E--> 526 ATGTTTTTTAA CACTATACTC TAAAATGGAC ATTTTCTTTT ATTATCAGTT
527 AAAATCACAT 2430
E--> 529 TTTAAGTGCT TCACATTTGT ATGTGTGTAG ACTGTAACCT TTTTTCAGTT
530 CATATGCAGA 2490
E--> 532 ACGTATTTAG CCATTACCCA CGTGACACCA CCGAATATAT TATCGATTTA
533 GAAGCAAAGA 2550
E--> 535 TTTCAGTAGA ATTTTAGTCC TGAACGCTAC GGGGAAAATG CATTTTCTTC
536 AGAATTATCC 2610
E--> 538 ATTACGTGCA TTTAACTCT GCCAGAAAAA AATAACTATT TTGTTTTAAT
539 CTACTTTTTG 2670
E--> 541 TATTTAGTAG TATTTGTAT AAATTAAATA AACTGTTTTG AAGTCAAAAA AAAA
W--> 542 2724

```

*Unappreciated
nucleotides*

621 (2) INFORMATION FOR SEQ ID NO: 5:

622 (i) SEQUENCE CHARACTERISTICS:

623 (A) LENGTH: 2932 base pairs

624 (B) TYPE: nucleic acid

625 (C) STRANDEDNESS: unknown

626 (D) TOPOLOGY: linear

628 (ii) MOLECULE TYPE: cDNA

630 (iii) HYPOTHETICAL: NO

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C--> 632      (iv) ANTI-SENSE: NO
      634      (v) FRAGMENT TYPE: internal
      636      (vi) ORIGINAL SOURCE:
      637          (A) ORGANISM: Homo sapiens
      639      (ix) FEATURE:
      640          (A) NAME/KEY: CDS
      641          (B) LOCATION: 310..1905
      643      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
E--> 645 GCTCCGCGCC GAGGGCTGGA GGATGCGTTC CCTGGGGTCC GGACTTATGA
      646 AAATATGCAT      60
E--> 648 CAGTTTAATA CTGTCTTGGA ATTCATGAGA TGGAAGCATA GGTCAAAGCT
      649 GTTTGGAGAA      120
E--> 651 AATCAGAAGT ACAGTTTTAT CTAGCCACAT CTTGGAGGAG TCGTAAGAAA
      652 GCAGTGGGAG      180
E--> 654 TTGAAGTCAT TGTCAAGTGC TTGCGATCTT TTACAAGAAA ATCTCACTGA
      655 ATGATAGTCA      240
E--> 657 TTTAAATTGG TGAAGTAGCA AGACCAATTA TTAAAGGTGA CAGTACACAG
      658 GAAACATTAC      300
      660 AATTGAACA ATG ACT CAG CTA TAC ATT TAC ATC AGA TTA TTG GGA GCC      348
      661      Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala
      662      1      5      10
      664 TAT TTG TTC ATC ATT TCT CGT GTT CAA GGA CAG AAT CTG GAT AGT ATG      396
      665 Tyr Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met
      666      15      20      25
      668 CTT CAT GGC ACT GGG ATG AAA TCA GAC TCC GAC CAG AAA AAG TCA GAA      444
      669 Leu His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu
      670      30      35      40      45
      672 AAT GGA GTA ACC TTA GCA CCA GAG GAT ACC TTG CCT TTT TTA AAG TGC      492
      673 Asn Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys
      674      50      55      60
      676 TAT TGC TCA GGG CAC TGT CCA GAT GAT GCT ATT AAT AAC ACA TGC ATA      540
      677 Tyr Cys Ser Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile
      678      65      70      75
      680 ACT AAT GGA CAT TGC TTT GCC ATC ATA GAA GAA GAT GAC CAG GGA GAA      588
      681 Thr Asn Gly His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu
      682      80      85      90
      684 ACC ACA TTA GCT TCA GGG TGT ATG AAA TAT GAA GGA TCT GAT TTT CAG      636
      685 Thr Thr Leu Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln
      686      95      100      105
      688 TGC AAA GAT TCT CCA AAA GCC CAG CTA CGC CGG ACA ATA GAA TGT TGT      684
      689 Cys Lys Asp Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys
      690      110      115      120      125
      692 CGG ACC AAT TTA TGT AAC CAG TAT TTG CAA CCC ACA CTG CCC CCT GTT      732
      693 Arg Thr Asn Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val
      694      130      135      140
      696 GTC ATA GGT CCG TTT TTT GAT GGC AGC ATT CGA TGG CTG GTT TTG CTC      780
      697 Val Ile Gly Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu
      698      145      150      155
      700 ATT TCT ATG GCT GTC TGC ATA ATT GCT ATG ATC ATC TTC TCC AGC TGC      828

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701	Ile	Ser	Met	Ala	Val	Cys	Ile	Ile	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	
702			160						165				170				
704	TTT	TGT	TAC	AAA	CAT	TAT	TGC	AAG	AGC	ATC	TCA	AGC	AGA	CGT	CGT	TAC	876
705	Phe	Cys	Tyr	Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Arg	Arg	Tyr	
706			175						180				185				
708	AAT	CGT	GAT	TTG	GAA	CAG	GAT	GAA	GCA	TTT	ATT	CCA	GTT	GGA	GAA	TCA	924
709	Asn	Arg	Asp	Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	
710	190					195					200					205	
712	CTA	AAA	GAC	CTT	ATT	GAC	CAG	TCA	CAA	AGT	TCT	GGT	AGT	GGG	TCT	GGA	972
713	Leu	Lys	Asp	Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	
714				210					215						220		
716	CTA	CCT	TTA	TTG	GTT	CAG	CGA	ACT	ATT	GCC	AAA	CAG	ATT	CAG	ATG	GTC	1020
717	Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	
718				225					230					235			
E-->	720	CGG	CAA	GTT	GGT	AAA	GGC	CGA	TAT	GGA	GAA	GTA	TGG	ATG	GGC	AAA	TGG
W-->	721	1068															
	722	Arg	Gln	Val	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp
W-->	723		240						245				250				
	725	CGT	GGC	GAA	AAA	GTG	GCG	GTG	AAA	GTA	TTC	TTT	ACC	ACT	GAA	GAA	GCC
	726	Arg	Gly	Glu	Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala
W-->	727		255						260				265				
	729	AGC	TGG	TTT	CGA	GAA	ACA	GAA	ATC	TAC	CAA	ACT	GTG	CTA	ATG	CGC	CAT
	730	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His
W-->	731	270				275				280			285				
	733	GAA	AAC	ATA	CTT	GGT	TTC	ATA	GCG	GCA	GAC	ATT	AAA	GGT	ACA	GGT	TCC
	734	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser
W-->	735			290					295				300				
	737	TGG	ACT	CAG	CTC	TAT	TTG	ATT	ACT	GAT	TAC	CAT	GAA	AAT	GGA	TCT	CTC
	738	Trp	Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu
W-->	739			305					310				315				
	741	TAT	GAC	TTC	CTG	AAA	TGT	GCT	ACA	CTG	GAC	ACC	AGA	GCC	CTG	CTT	AAA
	742	Tyr	Asp	Phe	Leu	Lys	Cys	Ala	Thr	Leu	Asp	Thr	Arg	Ala	Leu	Leu	Lys
W-->	743		320						325				330				
	745	TTG	GCT	TAT	TCA	GCT	GCC	TGT	GGT	CTG	TGC	CAC	CTG	CAC	ACA	GAA	ATT
	746	Leu	Ala	Tyr	Ser	Ala	Ala	Cys	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile
W-->	747		335						340				345				
	749	TAT	GGC	ACC	CAA	GGA	AAG	CCC	GCA	ATT	GCT	CAT	CGA	GAC	CTA	AAG	AGC
	750	Tyr	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser
W-->	751	350				355				360			365				
	753	AAA	AAC	ATC	CTC	ATC	AAG	AAA	AAT	GGG	AGT	TGC	TGC	ATT	GCT	GAC	CTG
	754	Lys	Asn	Ile	Leu	Ile	Lys	Lys	Asn	Gly	Ser	Cys	Cys	Ile	Ala	Asp	Leu
W-->	755			370					375				380				
	757	GGC	CTT	GCT	GTT	AAA	TTC	AAC	AGT	GAC	ACA	AAT	GAA	GTT	GAT	GTG	CCC
	758	Gly	Leu	Ala	Val	Lys	Phe	Asn	Ser	Asp	Thr	Asn	Glu	Val	Asp	Val	Pro
W-->	759			385					390				395				
	761	TTG	AAT	ACC	AGG	GTG	GGC	ACC	AAA	CGC	TAC	ATG	GCT	CCC	GAA	GTG	CTG
	762	Leu	Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu
W-->	763		400						405				410				
	765	GAC	GAA	AGC	CTG	AAC	AAA	AAC	CAC	TTC	CAG	CCC	TAC	ATC	ATG	GCT	GAC
																	1596

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766 Asp Glu Ser Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp
W--> 767      415              420              425
769 ATC TAC AGC TTC GGC CTA ATC ATT TGG GAG ATG GCT CGT CGT TGT ATC      1644
770 Ile Tyr Ser Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile
W--> 771 430              435              440              445
773 ACA GGA GGG ATC GTG GAA GAA TAC CAA TTG CCA TAT TAC AAC ATG GTA      1692
774 Thr Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val
W--> 775              450              455              460
777 CCG AGT GAT CCG TCA TAC GAA GAT ATG CGT GAG GTT GTG TGT GTC AAA      1740
778 Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys
W--> 779              465              470              475
781 CGT TTG CGG CCA ATT GTG TCT AAT CGG TGG AAC AGT GAT GAA TGT CTA      1788
782 Arg Leu Arg Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu
W--> 783              480              485              490
785 CGA GCA GTT TTG AAG CTA ATG TCA GAA TGC TGG GCC CAC AAT CCA GCC      1836
786 Arg Ala Val Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala
W--> 787              495              500              505
789 TCC AGA CTC ACA GCA TTG AGA ATT AAG AAG ACG CTT GCC AAG ATG GTT      1884
790 Ser Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val
W--> 791 510              515              520              525
E--> 793 GAA TCC CAA GAT GTA AAA ATC TGATGGTTAA ACCATCGGAG GAGAAACTCT
W--> 794 1935
795 Glu Ser Gln Asp Val Lys Ile
W--> 796              530
E--> 798 AGACTGCAAG AACTGTTTTT ACCCATGGCA TGGGTGGAAT TAGAGTGGAA
799 TAAGGATGTT      1995
E--> 801 AACTTGTTTC TCAGACTCTT TCTTCACTAC GTGTTCACAG GCTGCTAATA
802 TTAAACCTTT      2055
E--> 804 CAGTACTCTT ATTAGGATAC AAGCTGGGAA CTTCTAAACA CTTCAATTCTT
805 TATATATGGA      2115
E--> 807 CAGCTTTTATT TTAAATGTGG TTTTGTGATGC CTTTTTTTAA GTGGGTTTTT
808 ATGAACTGCA      2175
E--> 810 TCAAGACTTC AATCCTGATT AGTGTCTCCA GTCAAGCTCT GGGTACTGAA
811 TTGCCTGTTC      2235
E--> 813 ATAAAACGGT GCTTTCTGTG AAAGCCTTAA GAAGATAAAT GAGCGCAGCA
814 GAGATGGAGA      2295
E--> 816 AATAGACTTT GCCTTTTACC TGAGACATTC AGTTCGTTTG TATTCTACCT
817 TTGTAAACA      2355
E--> 819 GCCTATAGAT GATGATGTGT TTGGGATACT GCTTATTTTA TGATAGTTTG
820 TCCTGTGTCC      2415
E--> 822 TTAGTGATGT GTGTGTGTCT CCATGCACAT GCACGCCGGG ATTCCTCTGC
823 TGCCATTTGA      2475
E--> 825 ATTAGAAGAA AATAATTTAT ATGCATGCAC AGGAAGATAT TGGTGGCCGG
826 TGGTTTTGTG      2535
E--> 828 CTTTAAAAAT GCAATATCTG ACCAAGATTC GCCAATCTCA TACAAGCCAT
829 TTAATTTGCA      2595
E--> 831 AGTGAGATAG CTTCCCCACC AGCTTTATTT TTTAACATGA AAGCTGATGC
832 CAAGGCCAAA      2655
E--> 834 AGAAGTTTAA AGCATCTGTA AATTGGACT GTTTTCCTTC AACCACCATT

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835 TTTTTTGTGG      2715
E--> 837 TTATTATTTT TGTACGGAA AGCATCCTCT CCAAAGTTGG AGCTTCTATT
      838 GCCATGAACC      2775
E--> 840 ATGCTTACAA AGAAAGCACT TCTTATTGAA GTGAATTCCT GCATTTGATA
      841 GCAATGTAAG      2835
E--> 843 TGCCTATAAC CATGTTCTAT ATTCTTTATT CTCAGTAACT TTAAAAAGGG
      844 AAGTTATTTA      2895
      846 TATTTTGTGT ATAATGTGCT TTATTTGCAA ATCACCC      2932
929 (2) INFORMATION FOR SEQ ID NO: 7:
930 (i) SEQUENCE CHARACTERISTICS:
931 (A) LENGTH: 2333 base pairs
932 (B) TYPE: nucleic acid
933 (C) STRANDEDNESS: unknown
934 (D) TOPOLOGY: linear
936 (ii) MOLECULE TYPE: cDNA
938 (iii) HYPOTHETICAL: NO
C--> 940 (iv) ANTI-SENSE: NO
      942 (v) FRAGMENT TYPE: internal
      944 (vi) ORIGINAL SOURCE:
      945 (A) ORGANISM: Homo sapiens
      947 (ix) FEATURE:
      948 (A) NAME/KEY: CDS
      949 (B) LOCATION: 1..1515
951 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
953 ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT GTT GTC CTC      48
954 Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Pro Leu Val Val Leu
955 1 5 10 15
957 CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG GTC CAG GCT CTG      96
958 Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Val Gln Ala Leu
959 20 25 30
961 CTG TGT GCG TGC ACC AGC TGC CTC CAG GCC AAC TAC ACG TGT GAG ACA      144
962 Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr
963 35 40 45
965 GAT GGG GCC TGC ATG GTT TCC TTT TTC AAT CTG GAT GGG ATG GAG CAC      192
966 Asp Gly Ala Cys Met Val Ser Phe Phe Asn Leu Asp Gly Met Glu His
967 50 55 60
969 CAT GTG CGC ACC TGC ATC CCC AAA GTG GAG CTG GTC CCT GCC GGG AAG      240
970 His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys
971 65 70 75 80
973 CCC TTC TAC TGC CTG AGC TCG GAG GAC CTG CGC AAC ACC CAC TGC TGC      288
974 Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys
975 85 90 95
977 TAC ACT GAC TAC TGC AAC AGG ATC GAC TTG AGG GTG CCC AGT GGT CAC      336
978 Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His
979 100 105 110
981 CTC AAG GAG CCT GAG CAC CCG TCC ATG TGG GGC CCG GTG GAG CTG GTA      384
982 Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val
983 115 120 125
985 GGC ATC ATC GCC GGC CCG GTG TTC CTC CTG TTC CTC ATC ATC ATC ATT      432

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```

986 Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile
987      130      135      140
989 GTT TTC CTT GTC ATT AAC TAT CAT CAG CGT GTC TAT CAC AAC CGC CAG      480
990 Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln
991 145      150      155      160
993 AGA CTG GAC ATG GAA GAT CCC TCA TGT GAG ATG TGT CTC TCC AAA GAC      528
994 Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp
995      165      170      175
997 AAG ACG CTC CAG GAT CTT GTC TAC GAT CTC TCC ACC TCA GGG TCT GGC      576
998 Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly
999      180      185      190
1001 TCA GGG TTA CCC CTC TTT GTC CAG CGC ACA GTG GCC CGA ACC ATC GTT      624
1002 Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val
1003      195      200      205
1005 TTA CAA GAG ATT ATT GGC AAG GGT CGG TTT GGG GAA GTA TGG CGG GGC      672
1006 Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly
1007      210      215      220
1009 CGC TGG AGG GGT GGT GAT GTG GCT GTG AAA ATA TTC TCT TCT CGT GAA      720
1010 Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu
1011 225      230      235      240
1013 GAA CGG TCT TGG TTC AGG GAA GCA GAG ATA TAC CAG ACG GTC ATG CTG      768
1014 Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu
1015      245      250      255
1016 CGC CAT GAA AAC ATC CTT GGA TTT ATT GCT GCT GAC AAT AAA GAT AAT      816
1017 Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn
1018      260      265      270
1020 GGC ACC TGG ACA CAG CTG TGG CTT GTT TCT GAC TAT CAT GAG CAC GGC      864
1021 Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly
1022      275      280      285
1024 TCC CTG TTT GAT TAT CTG AAC CGG TAC ACA GTG ACA ATT GAG GGG ATG      912
1025 Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met
1026      290      295      300
1028 ATT AAG CTG GCC TTG TCT GCT GCT AGT GGG CTG GCA CAC CTG CAC ATG      960
1029 Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met
1030 305      310      315      320
1032 GAG ATC GTG GGC ACC CAA GGG AAG CCT GGA ATT GCT CAT CGA GAC TTA      1008
1033 Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu
1034      325      330      335
1036 AAG TCA AAG AAC ATT CTG GTG AAG AAA AAT GGC ATG TGT GCC ATA GCA      1056
1037 Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala
1038      340      345      350
1040 GAC CTG GGC CTG GCT GTC CGT CAT GAT GCA GTC ACT GAC ACC ATT GAC      1104
1041 Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp
1042      355      360      365
1044 ATT GCC CCG AAT CAG AGG GTG GGG ACC AAA CGA TAC ATG GCC CCT GAA      1152
1045 Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu
1046      370      375      380
1048 GTA CTT GAT GAA ACC ATT AAT ATG AAA CAC TTT GAC TCC TTT AAA TGT      1200
1049 Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys

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1050 385          390          395          400
1052 GCT GAT ATT TAT GCC CTC GGG CTT GTA TAT TGG GAG ATT GCT CGA AGA      1248
1053 Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg
1054          405          410          415
1056 TGC AAT TCT GGA GGA GTC CAT GAA GAA TAT CAG CTG CCA TAT TAC GAC      1296
1057 Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp
1058          420          425          430
1060 TTA GTG CCC TCT GAC CCT TCC ATT GAG GAG GAA ATG CGA AAG GTT GTA TGT      1344
1061 Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys
1062          435          440          445
1064 GAT CAG AAG CTG CGT CCC AAC ATC CCC AAC TGG TGG CAG AGT TAT GAG      1392
1065 Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu
1066          450          455          460
1068 GCA CTG CGG GTG ATG GGG AAG ATG ATG CGA GAG TGT TGG TAT GCC AAC      1440
1069 Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn
1070 465          470          475          480
1072 GGC GCA GCC CGC CTG ACG GCC CTG CGC ATC AAG AAG ACC CTC TCC CAG      1488
1073 Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln
1074          485          490          495
1076 CTC AGC GTG CAG GAA GAC GTG AAG ATC TAACTGCTCC CTCTCTCCAC      1535
1077 Leu Ser Val Gln Glu Asp Val Lys Ile
1078          500          505
E--> 1080 ACGGAGCTCC TGGCAGCGAG AACTACGCAC AGCTGCCGCG TTGAGCGTAC
1081 GATGGAGGCC      1595
E--> 1083 TACCTCTCGT TTCTGCCCAG CCCTCTGTGG CCAGGAGCCC TGGCCCGCAA
1084 GAGGGACAGA      1655
E--> 1086 GCCCGGGAGA GACTCGCTCA CTCCCATGTT GGGTTTGAGA CAGACACCTT
1087 TTCTATTTAC      1715
E--> 1089 CTCCTAATGG CATGGAGACT CTGAGAGCGA ATTGTGTGGA GAACTCAGTG
1090 CCACACCTCG      1775
E--> 1092 AACTGGTTGT AGTGGGAAGT CCCGCGAAAC CCGGTGCATC TGGCACGTGG
1093 CCAGGAGCCA      1835
E--> 1095 TGACAGGGGC GCTTGGGAGG GGCCGGAGGA ACCGAGGTGT TGCCAGTGCT
1096 AAGCTGCCCT      1895
E--> 1098 GAGGGTTTCC TTCGGGGACC AGCCCACAGC ACACCAAGGT GGCCCGGAAG
1099 AACCAGAAGT      1955
E--> 1101 GCAGCCCCTC TCACAGGCAG CTCTGAGCCG CGCTTTCCCC TCCTCCCTGG
1102 GATGGACGCT      2015
E--> 1104 GCCGGGAGAC TGCCAGTGGA GACGGAATCT GCCGCTTTGT CTGTCCAGCC
1105 GTGTGTGCAT      2075
E--> 1107 GTGCCGAGGT GCGTCCCCCG TTGTGCCTGG TTCGTGCCAT GCCCTTACAC
1108 GTGCGTGTGA      2135
E--> 1110 GTGTGTGTGT GTGTCTGTAG GTGCGCACTT ACCTGCTTGA GCTTTCTGTG
1111 CATGTGCAGG      2195
E--> 1113 TCGGGGGTGT GGTCTGTCATG CTGTCCGTGC TTGCTGGTGC CTCTTTTCAG
1114 TAGTGAGCAG      2255
E--> 1116 CATCTAGTTT CCCTGGTGCC CTTCCCTGGA GGTCTCTCCC TCCCCCAGAG
1117 CCCCTCATGC      2315
1119 CACAGTGGTA CTCTGTGT

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TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt

Output Set: N:\CRF3\10152001\I039177D.raw

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1199 (2) INFORMATION FOR SEQ ID NO: 9:
1200     (i) SEQUENCE CHARACTERISTICS:
1201         (A) LENGTH: 2308 base pairs
1202         (B) TYPE: nucleic acid
1203         (C) STRANDEDNESS: unknown
1204         (D) TOPOLOGY: linear
1206     (ii) MOLECULE TYPE: cDNA
1208     (iii) HYPOTHETICAL: NO
C--> 1210     (iv) ANTI-SENSE: NO
1212         (v) FRAGMENT TYPE: internal
1214     (vi) ORIGINAL SOURCE:
1215         (A) ORGANISM: Mouse
1217     (ix) FEATURE:
1218         (A) NAME/KEY: CDS
1219         (B) LOCATION: 77..1585
1221     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
E--> 1223 GGCAGAGCGA GGTITGCTGG GGTGAGGCAG CGGCGCGGCC GGGCCGGGCC
1224 GGGCCACAGG      60
E--> 1226 CGGTGGCGGC GGGACC ATG GAG GCG GCG GTC GCT GCT CCG CGT CCC CGG
W--> 1227 109
1228             Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg
1229             1             5             10
1231 CTG CTC CTC CTC GTG CTG GCG GCG GCG GCG GCG GCG GCG GCG CTG      157
1232 Leu Leu Leu Leu Val Leu Ala Ala Ala Ala Ala Ala Ala Ala Ala Leu
1233             15             20             25
1235 CTC CCG GGG GCG ACG GCG TTA CAG TGT TTC TGC CAC CTC TGT ACA AAA      205
1236 Leu Pro Gly Ala Thr Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys
1237             30             35             40
1239 GAC AAT TTT ACT TGT GTG ACA GAT GGG CTC TGC TTT GTC TCT GTC ACA      253
1240 Asp Asn Phe Thr Cys Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr
1241             45             50             55
1243 GAG ACC ACA GAC AAA GTT ATA CAC AAC AGC ATG TGT ATA GCT GAA ATT      301
1244 Glu Thr Thr Asp Lys Val Ile His Asn Ser Met Cys Ile Ala Glu Ile
1245             60             65             70             75
1247 GAC TTA ATT CCT CGA GAT AGG CCG TTT GTA TGT GCA CCC TCT TCA AAA      349
1248 Asp Leu Ile Pro Arg Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys
1249             80             85             90
1251 ACT GGG TCT GTG ACT ACA ACA TAT TGC TGC AAT CAG GAC CAT TGC AAT      397
1252 Thr Gly Ser Val Thr Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn
1253             95             100            105
1255 AAA ATA GAA CTT CCA ACT ACT GTA AAG TCA TCA CCT GGC CTT GGT CCT      445
1256 Lys Ile Glu Leu Pro Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro
1257             110            115            120
1259 GTG GAA CTG GCA GCT GTC ATT GCT GGA CCA GTG TGC TTC GTC TGC ATC      493
1260 Val Glu Leu Ala Ala Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile
1261             125            130            135
1263 TCA CTC ATG TTG ATG GTC TAT ATC TGC CAC AAC CGC ACT GTC ATT CAC      541
1264 Ser Leu Met Leu Met Val Tyr Ile Cys His Asn Arg Thr Val Ile His
1265 140            145            150            155

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1267	CAT	CGA	GTG	CCA	AAT	GAA	GAG	GAC	CCT	TCA	TTA	GAT	CGC	CCT	TTT	ATT	589
1268	His	Arg	Val	Pro	Asn	Glu	Glu	Asp	Pro	Ser	Leu	Asp	Arg	Pro	Phe	Ile	
1269					160					165					170		
1271	TCA	GAG	GGT	ACT	ACG	TTG	AAA	GAC	TTA	ATT	TAT	GAT	ATG	ACA	ACG	TCA	637
1272	Ser	Glu	Gly	Thr	Thr	Leu	Lys	Asp	Leu	Ile	Tyr	Asp	Met	Thr	Thr	Ser	
1273					175					180					185		
1275	GGT	TCT	GGC	TCA	GGT	TTA	CCA	TTG	CTT	GTT	CAG	AGA	ACA	ATT	GCG	AGA	685
1276	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Arg	
1277					190					195					200		
1279	ACT	ATT	GTG	TTA	CAA	GAA	AGC	ATT	GGC	AAA	GGT	CGA	TTT	GGA	GAA	GTT	733
1280	Thr	Ile	Val	Leu	Gln	Glu	Ser	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	
1281					205					210					215		
1283	TGG	AGA	GGA	AAG	TGG	CGG	GGA	GAA	GAA	GTT	GCT	GTT	AAG	ATA	TTC	TCC	781
1284	Trp	Arg	Gly	Lys	Trp	Arg	Gly	Glu	Glu	Val	Ala	Val	Lys	Ile	Phe	Ser	
1285	220					225						230				235	
1287	TCT	AGA	GAA	GAA	CGT	TCG	TGG	TTC	CGT	GAG	GCA	GAG	ATT	TAT	CAA	ACT	829
1288	Ser	Arg	Glu	Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	
1289					240					245					250		
1291	GTA	ATG	TTA	CGT	CAT	GAA	AAC	ATC	CTG	GGA	TTT	ATA	GCA	GCA	GAC	AAT	877
1292	Val	Met	Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	
1293					255					260					265		
1295	AAA	GAC	AAT	GGT	ACT	TGG	ACT	CAG	CTC	TGG	TTG	GTG	TCA	GAT	TAT	CAT	925
1296	Lys	Asp	Asn	Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	
1297					270					275					280		
1299	GAG	CAT	GGA	TCC	CTT	TTT	GAT	TAC	TTA	AAC	AGA	TAC	ACA	GTT	ACT	GTG	973
1300	Glu	His	Gly	Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Val	
1301					285					290					295		
1303	GAA	GGA	ATG	ATA	AAA	CTT	GCT	CTG	TCC	ACG	GCG	AGC	GGT	CTT	GCC	CAT	1021
1304	Glu	Gly	Met	Ile	Lys	Leu	Ala	Leu	Ser	Thr	Ala	Ser	Gly	Leu	Ala	His	
1305	300					305						310				315	
1307	CTT	CAC	ATG	GAG	ATT	GTT	GGT	ACC	CAA	GGA	AAG	CCA	GCC	ATT	GCT	CAT	1069
1308	Leu	His	Met	Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	
1309					320							325				330	
1311	AGA	GAT	TTG	AAA	TCA	AAG	AAT	ATC	TTG	GTA	AAG	AAG	AAT	GGA	ACT	TGC	1117
1312	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	
1313					335					340					345		
1315	TGT	ATT	GCA	GAC	TTA	GGA	CTG	GCA	GTA	AGA	CAT	GAT	TCA	GCC	ACA	GAT	1165
1316	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ser	Ala	Thr	Asp	
1317					350					355					360		
1319	ACC	ATT	GAT	ATT	GCT	CCA	AAC	CAC	AGA	GTG	GGA	ACA	AAA	AGG	TAC	ATG	1213
1320	Thr	Ile	Asp	Ile	Ala	Pro	Asn	His	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	
1321					365					370					375		
1323	GCC	CCT	GAA	GTT	CTC	GAT	GAT	TCC	ATA	AAT	ATG	AAA	CAT	TTT	GAA	TCC	1261
1324	Ala	Pro	Glu	Val	Leu	Asp	Asp	Ser	Ile	Asn	Met	Lys	His	Phe	Glu	Ser	
1325	380					385						390				395	
1327	TTC	AAA	CGT	GCT	GAC	ATC	TAT	GCA	ATG	GGC	TTA	GTA	TTC	TGG	GAA	ATT	1309
1328	Phe	Lys	Arg	Ala	Asp	Ile	Tyr	Ala	Met	Gly	Leu	Val	Phe	Trp	Glu	Ile	
1329					400					405					410		
1331	GCT	CGA	CGA	TGT	TCC	ATT	GGT	GGA	ATT	CAT	GAA	GAT	TAC	CAA	CTG	CCT	1357

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1332 Ala Arg Arg Cys Ser Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro
1333          415          420          425
1335 TAT TAT GAT CTT GTA CCT TCT GAC CCA TCA GTT GAA GAA ATG AGA AAA      1405
1336 Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys
1337          430          435          440
1339 GTT GTT TGT GAA CAG AAG TTA AGG CCA AAT ATC CCA AAC AGA TGG CAG      1453
1340 Val Val Cys Glu Gln Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln
1341          445          450          455
1343 AGC TGT GAA GCC TTG AGA GTA ATG GCT AAA ATT ATG AGA GAA TGT TGG      1501
1344 Ser Cys Glu Ala Leu Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp
1345 460          465          470          475
1347 TAT GCC AAT GGA GCA GCT AGG CTT ACA GCA TTG CGG ATT AAG AAA ACA      1549
1348 Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr
1349          480          485          490
1351 TTA TCG CAA CTC AGT CAA CAG GAA GGC ATC AAA ATG TAATTCTACA      1595
1352 Leu Ser Gln Leu Ser Gln Gln Glu Gly Ile Lys Met
1353          495          500
E--> 1355 GCTTTGCCTG AACTCTCCTT TTTTCTTCAG ATCTGCTCCT GGGTTTTAAT
1356 TTGGGAGGTC      1655
E--> 1358 AGTTGTTCTA CCTCACTGAG AGGGAACAGA AGGATATTGC TTCCTTTTGC
1359 AGCAGTGTA      1715
E--> 1361 TAAAGTCAAT TAAAACTTC CCAGGATTTT TTTGGACCCA GGAAACAGCC
1362 ATGTGGGTCC      1775
E--> 1364 TTTCTGTGCA CTATGAACGC TTCTTTCCCA GGACAGAAAA TGTGTAGTCT
1365 ACCTTTATTT      1835
E--> 1367 TTTATTAACA AAACCTTGTTT TTTAAAAAGA TGATTGCTGG TCTTAACTTT
1368 AGGTAACCT      1895
E--> 1370 GCTGTGCTGG AGATCATCTT TAAGGGCAAA GGAGTTGGAT TGCTGAATTA
1371 CAATGAAACA      1955
E--> 1373 TGTCTTATTA CTAAAGAAAG TGATTTACTC CTGGTTAGTA CATTCTCAGA
1374 GGATTCTGAA      2015
E--> 1376 CCACTAGAGT TTCCTTGATT CAGACTTTGA ATGTACTGTT CTATAGTTTT
1377 TCAGGATCTT      2075
E--> 1379 AAAACTAACA CTTATAAAAC TCTTATCTTG AGTCTAAAAA TGACCTCATA
1380 TAGTAGTGAG      2135
E--> 1382 GAACATAATT CATGCAATTG TATTTTGTAT ACTATTATTG TTCTTTCACT
1383 TATTCAGAAC      2195
E--> 1385 ATTACATGCC TTCAAAATGG GATTGTACTA TACCAGTAAG TGCCACTTCT
1386 GTGTCTTTCT      2255
E--> 1388 AATGGAAATG AGTAGAATTG CTGAAAGTCT CTATGTTAAA ACCTATAGTG TTT
W--> 1389      2308
1468 (2) INFORMATION FOR SEQ ID NO: 11:
1469 (i) SEQUENCE CHARACTERISTICS:
1470 (A) LENGTH: 1922 base pairs
1471 (B) TYPE: nucleic acid
1472 (C) STRANDEDNESS: unknown
1473 (D) TOPOLOGY: linear
1475 (ii) MOLECULE TYPE: cDNA
1477 (iii) HYPOTHETICAL: NO

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C--> 1479      (iv) ANTI-SENSE: NO
      1481      (v) FRAGMENT TYPE: internal
      1483      (vi) ORIGINAL SOURCE:
      1484          (A) ORGANISM: Mouse
      1486      (ix) FEATURE:
      1487          (A) NAME/KEY: CDS
      1488          (B) LOCATION: 241..1746
      1490      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
E--> 1492 GAGAGCACAG CCCTTCCCAG TCCCCGGAGC CGCCGCGCCA CGCGCGCATG
      1493 ATCAAGACCT      60
E--> 1495 TTTCCCCGGC CCCACAGGGC CTCTGGACGT GAGACCCCGG CCGCCTCCGC
      1496 AAGGAGAGGC      120
E--> 1498 GGGGGTCGAG TCGCCCTGTC CAAAGGCCTC AATCTAAACA ATCTTGATTC
      1499 CTGTTGCCGG      180
E--> 1501 CTGGCGGGAC CCTGAATGGC AGGAAATCTC ACCACATCTC TTCTCCTATC
      1502 TCCAAGGACC      240
      1504 ATG ACC TTG GGG AGC TTC AGA AGG GGC CTT TTG ATG CTG TCG GTG GCC      288
      1505 Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Leu Met Leu Ser Val Ala
      1506 1 5 10 15
      1508 TTG GGC CTA ACC CAG GGG AGA CTT GCG AAG CCT TCC AAG CTG GTG AAC      336
      1509 Leu Gly Leu Thr Gln Gly Arg Leu Ala Lys Pro Ser Lys Leu Val Asn
      1510 20 25 30
      1512 TGC ACT TGT GAG AGC CCA CAC TGC AAG AGA CCA TTC TGC CAG GGG TCA      384
      1513 Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser
      1514 35 40 45
      1516 TGG TGC ACA GTG GTG CTG GTT CGA GAG CAG GGC AGG CAC CCC CAG GTC      432
      1517 Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val
      1518 50 55 60
      1520 TAT CGG GGC TGT GGG AGC CTG AAC CAG GAG CTC TGC TTG GGA CGT CCC      480
      1521 Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro
      1522 65 70 75 80
      1524 ACG GAG TTT CTG AAC CAT CAC TGC TGC TAT AGA TCC TTC TGC AAC CAC      528
      1525 Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His
      1526 85 90 95
      1528 AAC GTG TCT CTG ATG CTG GAG GCC ACC CAA ACT CCT TCG GAG GAG CCA      576
      1529 Asn Val Ser Leu Met Leu Glu Ala Thr Gln Thr Pro Ser Glu Glu Pro
      1530 100 105 110
      1532 GAA GTT GAT GCC CAT CTG CCT CTG ATC CTG GGT CCT GTG CTG GCC TTG      624
      1533 Glu Val Asp Ala His Leu Pro Leu Ile Leu Gly Pro Val Leu Ala Leu
      1534 115 120 125
      1536 CCG GTC CTG GTG GCC CTG GGT GCT CTG GGC TTG TGG CGT GTC CGG CGG      672
      1537 Pro Val Leu Val Ala Leu Gly Ala Leu Gly Leu Trp Arg Val Arg Arg
      1538 130 135 140
      1540 AGG CAG GAG AAG CAG CGG GAT TTG CAC AGT GAC CTG GGC GAG TCC AGT      720
      1541 Arg Gln Glu Lys Gln Arg Asp Leu His Ser Asp Leu Gly Glu Ser
      1542 145 150 155 160
      1544 CTC ATC CTG AAG GCA TCT GAA CAG GCA GAC AGC ATG TTG GGG GAC TTC      768
      1545 Leu Ile Leu Lys Ala Ser Glu Gln Ala Asp Ser Met Leu Gly Asp Phe
      1546 165 170 175

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1548	CTG	GAC	AGC	GAC	TGT	ACC	ACG	GGC	AGC	GGC	TCG	GGG	CTC	CCC	TTC	TTG	816
1549	Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu	
1550				180					185					190			
1552	GTG	CAG	AGG	ACG	GTA	GCT	CGG	CAG	GTT	GCG	CTG	GTA	GAG	TGT	GTG	GGA	864
1553	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly	
1554				195				200						205			
1556	AAG	GGC	CGA	TAT	GGC	GAG	GTG	TGG	CGC	GGT	TCG	TGG	CAT	GGC	GAA	AGC	912
1557	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Ser	Trp	His	Gly	Glu	Ser	
1558		210					215					220					
1560	GTG	GCG	GTC	AAG	ATT	TTC	TCC	TCA	CGA	GAT	GAG	CAG	TCC	TGG	TTC	CGG	960
1561	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	Arg	
1562	225					230					235					240	
1564	GAG	ACG	GAG	ATC	TAC	AAC	ACA	GTT	CTG	CTT	AGA	CAC	GAC	AAC	ATC	CTA	1008
1565	Glu	Thr	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	Leu	
1566				245						250					255		
1568	GGC	TTC	ATC	GCC	TCC	GAC	ATG	ACT	TCG	CGG	AAC	TCG	AGC	ACG	CAG	CTG	1056
1569	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	Leu	
1570				260					265					270			
1572	TGG	CTC	ATC	ACC	CAC	TAC	CAT	GAA	CAC	GGC	TCC	CTC	TAT	GAC	TTT	CTG	1104
1573	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	Leu	
1574			275					280					285				
1576	CAG	AGG	CAG	ACG	CTG	GAG	CCC	CAG	TTG	GCC	CTG	AGG	CTA	GCT	GTG	TCC	1152
1577	Gln	Arg	Gln	Thr	Leu	Glu	Pro	Gln	Leu	Ala	Leu	Arg	Leu	Ala	Val	Ser	
1578		290					295				300						
1580	CCG	GCC	TGC	GGC	CTG	GCG	CAC	CTA	CAT	GTG	GAG	ATC	TTT	GGC	ACT	CAA	1200
1581	Pro	Ala	Cys	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	Gln	
1582	305				310					315					320		
1584	GGC	AAA	CCA	GCC	ATT	GCC	CAT	CGT	GAC	CTC	AAG	AGT	CGC	AAT	GTG	CTG	1248
1585	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Arg	Asn	Val	Leu	
1586				325					330						335		
1588	GTC	AAG	AGT	AAC	TTG	CAG	TGT	TGC	ATT	GCA	GAC	CTG	GGA	CTG	GCT	GTG	1296
1589	Val	Lys	Ser	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	
1590				340					345					350			
1592	ATG	CAC	TCA	CAA	AGC	AAC	GAG	TAC	CTG	GAT	ATC	GGC	AAC	ACA	CCC	CGA	1344
1593	Met	His	Ser	Gln	Ser	Asn	Glu	Tyr	Leu	Asp	Ile	Gly	Asn	Thr	Pro	Arg	
1594			355				360					365					
1596	GTG	GGT	ACC	AAA	AGA	TAC	ATG	GCA	CCC	GAG	GTG	CTG	GAT	GAG	CAC	ATC	1392
1597	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	His	Ile	
1598		370					375					380					
1600	CGC	ACA	GAC	TGC	TTT	GAG	TCG	TAC	AAG	TGG	ACA	GAC	ATC	TGG	GCC	TTT	1440
1601	Arg	Thr	Asp	Cys	Phe	Glu	Ser	Tyr	Lys	Trp	Thr	Asp	Ile	Trp	Ala	Phe	
1602	385					390					395					400	
1604	GGC	CTA	GTG	CTA	TGG	GAG	ATC	GCC	CGG	CGG	ACC	ATC	ATC	AAT	GGC	ATT	1488
1605	Gly	Leu	Val	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Thr	Ile	Ile	Asn	Gly	Ile	
1606				405						410					415		
1608	GTG	GAG	GAT	TAC	AGG	CCA	CCT	TTC	TAT	GAC	ATG	GTA	CCC	AAT	GAC	CCC	1536
1609	Val	Glu	Asp	Tyr	Arg	Pro	Pro	Phe	Tyr	Asp	Met	Val	Pro	Asn	Asp	Pro	
1610				420					425					430			
1612	AGT	TTT	GAG	GAC	ATG	AAA	AAG	GTG	GTG	TGC	GTT	GAC	CAG	CAG	ACA	CCC	1584

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1613 Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro
1614          435          440          445
1616 ACC ATC CCT AAC CGG CTG GCT GCA GAT CCG GTC CTC TCC GGG CTG GCC      1632
1617 Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala
1618    450          455          460
1620 CAG ATG ATG AGA GAG TGC TGG TAC CCC AAC CCC TCT GCT CGC CTC ACC      1680
1621 Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr
1622 465          470          475          480
1624 GCA CTG CGC ATA AAG AAG ACA TTG CAG AAG CTC AGT CAC AAT CCA GAG      1728
1625 Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu
1626          485          490          495
1628 AAG CCC AAA GTG ATT CAC TAGCCAGGG CCACCAGGCT TCCTCTGCCT      1776
1629 Lys Pro Lys Val Ile His
1630          500
E--> 1632 AAAGTGTGTG CTGGGGAAGA AGACATAGCC TGTCTGGGTA GAGGGAGTGA
1633 AGAGAGTGTG      1836
E--> 1635 CACGCTGCCC TGTGTGTGCC TGCTCAGCTT GCTCCCAGCC CATCCAGCCA
1636 AAAATACAGC      1896
1638 TGAGCTGAAA TTCAAAAAAA AAAAAA      1922
1716 (2) INFORMATION FOR SEQ ID NO: 13:
1717     (i) SEQUENCE CHARACTERISTICS:
1718         (A) LENGTH: 2070 base pairs
1719         (B) TYPE: nucleic acid
1720         (C) STRANDEDNESS: unknown
1721         (D) TOPOLOGY: linear
1723     (ii) MOLECULE TYPE: cDNA
1725     (iii) HYPOTHETICAL: NO
C--> 1727     (iv) ANTI-SENSE: NO
1729     (v) FRAGMENT TYPE: internal
1731     (vi) ORIGINAL SOURCE:
1732         (A) ORGANISM: Mouse
1734     (ix) FEATURE:
1735         (A) NAME/KEY: CDS
1736         (B) LOCATION: 217..1812
1738     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
E--> 1740 ATTCATGAGA TGGAAGCATA GGTCAAAGCT GTTCGGAGAA ATTGGAACTA
1741 CAGTTTTATC      60
E--> 1743 TAGCCACATC TCTGAGAATT CTGAAGAAAG CAGCAGGTGA AAGTCATTGC
1744 CAAGTGATTT      120
E--> 1746 TGTTCTGTAA GGAAGCCTCC CTCATTCACT TACACCAGTG AGACAGCAGG
1747 ACCAGTCATT      180
E--> 1749 CAAAGGGCCG TGTACAGGAC GCGTGGCAAT CAGACA ATG ACT CAG CTA TAC ACT
W--> 1750      234
1751          Met Thr Gln Leu Tyr Thr
1752          1          5
1754 TAC ATC AGA TTA CTG GGA GCC TGT CTG TTC ATC ATT TCT CAT GTT CAA      282
1755 Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe Ile Ile Ser His Val Gln
1756    10          15          20
1758 GGG CAG AAT CTA GAT AGT ATG CTC CAT GGC ACT GGT ATG AAA TCA GAC      330

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1759	Gly	Gln	Asn	Leu	Asp	Ser	Met	Leu	His	Gly	Thr	Gly	Met	Lys	Ser	Asp	
1760			25					30					35				
1762	TTG	GAC	CAG	AAG	AAG	CCA	GAA	AAT	GGA	GTG	ACT	TTA	GCA	CCA	GAG	GAT	378
1763	Leu	Asp	Gln	Lys	Lys	Pro	Glu	Asn	Gly	Val	Thr	Leu	Ala	Pro	Glu	Asp	
1764		40					45					50					
1766	ACC	TTG	CCT	TTC	TTA	AAG	TGC	TAT	TGC	TCA	GGA	CAC	TGC	CCA	GAT	GAT	426
1767	Thr	Leu	Pro	Phe	Leu	Lys	Cys	Tyr	Cys	Ser	Gly	His	Cys	Pro	Asp	Asp	
1768		55				60					65				70		
1770	GCT	ATT	AAT	AAC	ACA	TGC	ATA	ACT	AAT	GGC	CAT	TGC	TTT	GCC	ATT	ATA	474
1771	Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly	His	Cys	Phe	Ala	Ile	Ile	
1772				75					80						85		
1774	GAA	GAA	GAT	GAT	CAG	GGA	GAA	ACC	ACA	TTA	ACT	TCT	GGG	TGT	ATG	AAG	522
1775	Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu	Thr	Ser	Gly	Cys	Met	Lys	
1776			90					95					100				
1778	TAT	GAA	GGC	TCT	GAT	TTT	CAA	TGC	AAG	GAT	TCA	CCG	AAA	GCC	CAG	CTA	570
1779	Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp	Ser	Pro	Lys	Ala	Gln	Leu	
1780			105				110						115				
1782	CGC	AGG	ACA	ATA	GAA	TGT	TGT	CGG	ACC	AAT	TTG	TGC	AAC	CAG	TAT	TTG	618
1783	Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn	Leu	Cys	Asn	Gln	Tyr	Leu	
1784		120					125					130					
1786	CAG	CCT	ACA	CTG	CCC	CCT	GTT	GTT	ATA	GGT	CCG	TTC	TTT	GAT	GGC	AGC	666
1787	Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly	Pro	Phe	Phe	Asp	Gly	Ser	
1788	135				140					145					150		
1790	ATC	CGA	TGG	CTG	GTT	GTG	CTC	ATT	TCC	ATG	GCT	GTC	TGT	ATA	GTT	GCT	714
1791	Ile	Arg	Trp	Leu	Val	Val	Leu	Ile	Ser	Met	Ala	Val	Cys	Ile	Val	Ala	
1792			155						160					165			
1794	ATG	ATC	ATC	TTC	AGC	TGC	TTT	TGC	TAT	AAG	CAT	TAT	TGT	AAG	AGT		762
1795	Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr	Lys	His	Tyr	Cys	Lys	Ser	
1796			170				175					180					
1798	ATC	TCA	AGC	AGG	GGT	CGT	TAC	AAC	CGT	GAT	TTG	GAA	CAG	GAT	GAA	GCA	810
1799	Ile	Ser	Ser	Arg	Gly	Arg	Tyr	Asn	Arg	Asp	Leu	Glu	Gln	Asp	Glu	Ala	
1800			185				190					195					
1802	TTT	ATT	CCA	GTA	GGA	GAA	TCA	TTG	AAA	GAC	CTG	ATT	GAC	CAG	TCC	CAA	858
1803	Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp	Leu	Ile	Asp	Gln	Ser	Gln	
1804		200				205					210						
1806	AGC	TCT	GGG	AGT	GGA	TCT	GGA	TTG	CCT	TTA	TTG	GTT	CAG	CGA	ACT	ATT	906
1807	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	
1808	215				220					225					230		
1810	GCC	AAA	CAG	ATT	CAG	ATG	GTT	CGG	CAG	GTT	GGT	AAA	GGC	CGC	TAT	GGA	954
1811	Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val	Gly	Lys	Gly	Arg	Tyr	Gly	
1812			235						240					245			
1814	GAA	GTA	TGG	ATG	GGT	AAA	TGG	CGT	GGT	GAA	AAA	GTG	GCT	GTC	AAA	GTG	1002
1815	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu	Lys	Val	Ala	Val	Lys	Val	
1816			250					255					260				
1818	TTT	TTT	ACC	ACT	GAA	GAA	GCT	AGC	TGG	TTT	AGA	GAA	ACA	GAA	ATC	TAC	1050
1819	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	
1820			265				270					275					
1822	CAG	ACG	GTG	TTA	ATG	CGT	CAT	GAA	AAT	ATA	CTT	GGT	TTT	ATA	GCT	GCA	1098
1823	Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	

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Input Set : A:\Lud-5539 sequence listing.txt

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1824	280	285	290	
1826	GAC ATT AAA GGC ACT GGT TCC TGG ACT CAG CTG TAT TTG ATT ACT GAT	1146		
1827	Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp			
1828	295 300 305 310			
1830	TAC CAT GAA AAT GGA TCT CTC TAT GAC TTC CTG AAA TGT GCC ACA CTA	1194		
1831	Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe Leu Lys Cys Ala Thr Leu			
1832	315 320 325			
1834	GAC ACC AGA GCC CTA CTC AAG TTA GCT TAT TCT GCT GCT TGT GGT CTG	1242		
1835	Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr Ser Ala Ala Cys Gly Leu			
1836	330 335 340			
1838	TGC CAC CTC CAC ACA GAA ATT TAT GGT ACC CAA GGG AAG CCT GCA ATT	1290		
1839	Cys His Leu His Thr Glu Ile Tyr Gly Thr Gln Gly Lys Pro Ala Ile			
1840	345 350 355			
1842	GCT CAT CGA GAC CTG AAG AGC AAA AAC ATC CTT ATT AAG AAA AAT GGA	1338		
1843	Ala His Arg Asp Leu Lys Ser Lys Asn Ile Leu Ile Lys Lys Asn Gly			
1844	360 365 370			
1846	AGT TGC TGT ATT GCT GAC CTG GGC CTA GCT GTT AAA TTC AAC AGT GAT	1386		
1847	Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Lys Phe Asn Ser Asp			
1848	375 380 385 390			
1850	ACA AAT GAA GTT GAC ATA CCC TTG AAT ACC AGG GTG GGC ACC AAG CGG	1434		
1851	Thr Asn Glu Val Asp Ile Pro Leu Asn Thr Arg Val Gly Thr Lys Arg			
1852	395 400 405			
1854	TAC ATG GCT CCA GAA GTG CTG GAT GAA AGC CTG AAT AAA AAC CAT TTC	1482		
1855	Tyr Met Ala Pro Glu Val Leu Asp Glu Ser Leu Asn Lys Asn His Phe			
1856	410 415 420			
1858	CAG CCC TAC ATC ATG GCT GAC ATC TAT AGC TTT GGT TTG ATC ATT TGG	1530		
1859	Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser Phe Gly Leu Ile Ile Trp			
1860	425 430 435			
1862	GAA ATG GCT CGT CGT TGT ATT ACA GGA GGA ATC GTG GAG GAA TAT CAA	1578		
1863	Glu Met Ala Arg Arg Cys Ile Thr Gly Gly Ile Val Glu Glu Tyr Gln			
1864	440 445 450			
1866	TTA CCA TAT TAC AAC ATG GTG CCC AGT GAC CCA TCC TAT GAG GAC ATG	1626		
1867	Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp Pro Ser Tyr Glu Asp Met			
1868	455 460 465 470			
1870	CGT GAG GTT GTG TGT GTG AAA CGC TTG CGG CCA ATC GTG TCT AAC CGC	1674		
1871	Arg Glu Val Val Cys Val Lys Arg Leu Arg Pro Ile Val Ser Asn Arg			
1872	475 480 485			
1874	TGG AAC AGC GAT GAA TGT CTT CGA GCA GTT TTG AAG CTA ATG TCA GAA	1722		
1875	Trp Asn Ser Asp Glu Cys Leu Arg Ala Val Leu Lys Leu Met Ser Glu			
1876	490 495 500			
1878	TGT TGG GCC CAT AAT CCA GCC TCC AGA CTC ACA GCT TTG AGA ATC AAG	1770		
1879	Cys Trp Ala His Asn Pro Ala Ser Arg Leu Thr Ala Leu Arg Ile Lys			
1880	505 510 515			
1882	AAG ACA CTT GCA AAA ATG GTT GAA TCC CAG GAT GTA AAG ATT	1812		
1883	Lys Thr Leu Ala Lys Met Val Glu Ser Gln Asp Val Lys Ile			
1884	520 525 530			
E-->	1886 TGACAATTAA ACAATTTTGA GGGAGAATTT AGACTGCAAG AACTTCTTCA			
	1887 CCCAAGGAAT 1872			
E-->	1889 GGGTGGGATT AGCATGGAAT AGGATGTTGA CTGGGTTTCC AGACTCCTTC			

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1890 CTCTACATCT      1932
E--> 1892 TCACAGGCTG CTAACAGTAA ACCTTACCGT ACTCTACAGA ATACAAGATT
1893 GGAAC TTGGA      1992
E--> 1895 ACTTCAAACA TGTCATTCTT TATATATGAC AGCTTTGTTT TAATGTGGGG
1896 TTTTTTTGTT      2052
1898 TGCTTTTTTTT GTTTTGTGTT
1981 (2) INFORMATION FOR SEQ ID NO: 15:
1982 (i) SEQUENCE CHARACTERISTICS:
1983 (A) LENGTH: 2160 base pairs
1984 (B) TYPE: nucleic acid
1985 (C) STRANDEDNESS: unknown
1986 (D) TOPOLOGY: linear
1988 (ii) MOLECULE TYPE: cDNA
1990 (iii) HYPOTHETICAL: NO
C--> 1992 (iv) ANTI-SENSE: NO
1994 (v) FRAGMENT TYPE: internal
1996 (vi) ORIGINAL SOURCE:
1997 (A) ORGANISM: Mouse
1999 (ix) FEATURE:
2000 (A) NAME/KEY: CDS
2001 (B) LOCATION: 10..1524
2003 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
2005 CGCGGTTAC ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT      48
2006 Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu
2007 1 5 10
2009 GTT GTC CTC CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG ATC      96
2010 Val Val Leu Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Ile
2011 15 20 25
2013 CAG GCT CTG CTG TGT GCG TGC ACC AGC TGC CTA CAG ACC AAC TAC ACC      144
2014 Gln Ala Leu Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr
2015 30 35 40 45
2017 TGT GAG ACA GAT GGG GCT TGC ATG GTC TCC ATC TTT AAC CTG GAT GGC      192
2018 Cys Glu Thr Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly
2019 50 55 60
2021 GTG GAG CAC CAT GTA CGT ACC TGC ATC CCC AAG GTG GAG CTG GTT CCT      240
2022 Val Glu His His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro
2023 65 70 75
2025 GCT GGA AAG CCC TTC TAC TGC CTG AGT TCA GAG GAT CTG CGC AAC ACA      288
2026 Ala Gly Lys Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr
2027 80 85 90
2029 CAC TGC TGC TAT ATT GAC TTC TGC AAC AAG ATT GAC CTC AGG GTC CCC      336
2030 His Cys Cys Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro
2031 95 100 105
2033 AGC GGA CAC CTC AAG GAG CCT GCG CAC CCC TCC ATG TGG GGC CCT GTG      384
2034 Ser Gly His Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val
2035 110 115 120 125
2037 GAG CTG GTC GGC ATC ATC GCC GGC CCC GTC TTC CTC CTC TTC CTT ATC      432
2038 Glu Leu Val Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile
2039 130 135 140

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2041	ATT	ATC	ATC	GTC	TTC	CTG	GTC	ATC	AAC	TAT	CAC	CAG	CGT	GTC	TAC	CAT	480
2042	Ile	Ile	Ile	Val	Phe	Leu	Val	Ile	Asn	Tyr	His	Gln	Arg	Val	Tyr	His	
2043				145					150					155			
2045	AAC	CGC	CAG	AGG	TTG	GAC	ATG	GAG	GAC	CCC	TCT	TGC	GAG	ATG	TGT	CTC	528
2046	Asn	Arg	Gln	Arg	Leu	Asp	Met	Glu	Asp	Pro	Ser	Cys	Glu	Met	Cys	Leu	
2047				160					165					170			
2049	TCC	AAA	GAC	AAG	ACG	CTC	CAG	GAT	CTC	GTC	TAC	GAC	CTC	TCC	ACG	TCA	576
2050	Ser	Lys	Asp	Lys	Thr	Leu	Gln	Asp	Leu	Val	Tyr	Asp	Leu	Ser	Thr	Ser	
2051				175					180					185			
2053	GGG	TCT	GGC	TCA	GGG	TTA	CCC	CTT	TTT	GTC	CAG	CGC	ACA	GTG	GCC	CGA	624
2054	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	Phe	Val	Gln	Arg	Thr	Val	Ala	Arg	
2055	190						195				200					205	
2057	ACC	ATT	GTT	TTA	CAA	GAG	ATT	ATC	GGC	AAG	GGC	CGG	TTC	GGG	GAA	GTA	672
2058	Thr	Ile	Val	Leu	Gln	Glu	Ile	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	
2059					210					215					220		
2061	TGG	CGT	GGT	CGC	TGG	AGG	GGT	GGT	GAC	GTG	GCT	GTG	AAA	ATC	TTC	TCT	720
2062	Trp	Arg	Gly	Arg	Trp	Arg	Gly	Gly	Asp	Val	Ala	Val	Lys	Ile	Phe	Ser	
2063					225					230					235		
2065	TCT	CGT	GAA	GAA	CGG	TCT	TGG	TTC	CGT	GAA	GCA	GAG	ATC	TAC	CAG	ACC	768
2066	Ser	Arg	Glu	Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	
2067				240					245					250			
2069	GTC	ATG	CTG	CGC	CAT	GAA	AAC	ATC	CTT	GGC	TTT	ATT	GCT	GCT	GAC	AAT	816
2070	Val	Met	Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	
2071				255					260					265			
2073	AAA	GAT	AAT	GGC	ACC	TGG	ACC	CAG	CTG	TGG	CTT	GTC	TCT	GAC	TAT	CAC	864
2074	Lys	Asp	Asn	Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	
2075	270					275					280				285		
2077	GAG	CAT	GGC	TCA	CTG	TTT	GAT	TAT	CTG	AAC	CGC	TAC	ACA	GTG	ACC	ATT	912
2078	Glu	His	Gly	Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Ile	
2079					290					295					300		
2081	GAG	GGA	ATG	ATT	AAG	CTA	GCC	TTG	TCT	GCA	GCC	AGT	GGT	TTG	GCA	CAC	960
2082	Glu	Gly	Met	Ile	Lys	Leu	Ala	Leu	Ser	Ala	Ala	Ser	Gly	Leu	Ala	His	
2083				305						310					315		
2085	CTG	CAT	ATG	GAG	ATT	GTG	GGC	ACT	CAA	GGG	AAG	CCG	GGA	ATT	GCT	CAT	1008
2086	Leu	His	Met	Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Gly	Ile	Ala	His	
2087				320					325					330			
2089	CGA	GAC	TTG	AAG	TCA	AAG	AAC	ATC	CTG	GTG	AAA	AAA	AAT	GGC	ATG	TGT	1056
2090	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Met	Cys	
2091				335					340					345			
2093	GCC	ATT	GCA	GAC	CTG	GGC	CTG	GCT	GTC	CGT	CAT	GAT	GCG	GTC	ACT	GAC	1104
2094	Ala	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ala	Val	Thr	Asp	
2095	350					355					360				365		
2097	ACC	ATA	GAC	ATT	GCT	CCA	AAT	CAG	AGG	GTG	GGG	ACC	AAA	CGA	TAC	ATG	1152
2098	Thr	Ile	Asp	Ile	Ala	Pro	Asn	Gln	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	
2099					370						375				380		
2101	GCT	CCT	GAA	GTC	CTT	GAC	GAG	ACA	ATC	AAC	ATG	AAG	CAC	TTT	GAC	TCC	1200
2102	Ala	Pro	Glu	Val	Leu	Asp	Glu	Thr	Ile	Asn	Met	Lys	His	Phe	Asp	Ser	
2103				385						390					395		
2105	TTC	AAA	TGT	GCC	GAC	ATC	TAT	GCC	CTC	GGG	CTT	GTC	TAC	TGG	GAG	ATT	1248

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2106 Phe Lys Cys Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile
2107          400          405          410
2109 GCA CGA AGA TGC AAT TCT GGA GGA GTC CAT GAA GAC TAT CAA CTG CCG      1296
2110 Ala Arg Arg Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro
2111      415          420          425
2113 TAT TAC GAC TTA GTG CCC TCC GAC CCT TCC ATT GAG GAG ATG CGA AAG      1344
2114 Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys
2115 430          435          440          445
2117 GTT GTA TGT GAC CAG AAG CTA CGG CCC AAT GTC CCC AAC TGG TGG CAG      1392
2118 Val Val Cys Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln
2119          450          455          460
2121 AGT TAT GAG GCC TTG CGA GTG ATG GGA AAG ATG ATG CGG GAG TGC TGG      1440
2122 Ser Tyr Glu Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp
2123          465          470          475
2125 TAC GCC AAT GGT GCT GCC CGT CTG ACA GCT CTG CGC ATC AAG AAG ACT      1488
2126 Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr
2127          480          485          490
2129 CTG TCC CAG CTA AGC GTG CAG GAA GAT GTG AAG ATT TAAGCTGTTC      1534
2130 Leu Ser Gln Leu Ser Val Gln Glu Asp Val Lys Ile
2131      495          500          505
E--> 2133 CTCTGCCTAC ACAAAGAACC TGGGCAGTGA GGATGACTGC AGCCACCGTG
2134 CAAGCGTCGT      1594
E--> 2136 GGAGGCCTAT CCTCTTGTTC CTGCCCCGCC CTCTGGCAGA GCCCTGGCCT
2137 GCAAGAGGGA      1654
E--> 2139 CAGAGCCTGG GAGACGCGCG CACTCCCGTT GGGTTTGAGA CAGACACTTT
2140 TTATATTTAC      1714
E--> 2142 CTCCTGATGG CATGGAGACC TGAGCAAATC ATGTAGTCAC TCAATGCCAC
2143 AACTCAAAC      1774
E--> 2145 GCTTCAGTGG GAAGTACAGA GACCCAGTGC ATTGCGTGTG CAGGAGCGTG
2146 AGGTGCTGGG      1834
E--> 2148 CTCGCCAGGA GCGGCCCCCA TACCTTGTGG TCCACTGGGC TGCAGGTTTT
2149 CCTCCAGGGA      1894
E--> 2151 CCAGTCAACT GGCATCAAGA TATTGAGAGG AACCGGAAGT TTCTCCCTCC
2152 TTCCCGTAGC      1954
E--> 2154 AGTCCTGAGC CACACCATCC TTCTCATGGA CATCCGGAGG ACTGCCCCCTA
2155 GAGACACAAC      2014
E--> 2157 CTGCTGCCTG TCTGTCCAGC CAAGTGCGCA TGTGCCGAGG TGTGTCCCAC
2158 ATTGTGCCTG      2074
E--> 2160 GTCTGTGCCA CGCCCGTGTG TGTGTGTGTG TGTGTGAGTG AGTGTGTGTG
2161 TGTACACTTA      2134
2163 ACCTGCTTGA GCTTCTGTGC ATGTGT      2160
2242 (2) INFORMATION FOR SEQ ID NO: 17:
2243 (i) SEQUENCE CHARACTERISTICS:
2244 (A) LENGTH: 1952 base pairs
2245 (B) TYPE: nucleic acid
2246 (C) STRANDEDNESS: unknown
2247 (D) TOPOLOGY: unknown
2249 (ii) MOLECULE TYPE: cDNA
2251 (iii) HYPOTHETICAL: NO

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C--> 2253      (iv) ANTI-SENSE: NO
      2255      (v) FRAGMENT TYPE: internal
      2257      (vi) ORIGINAL SOURCE:
      2258          (A) ORGANISM: Mouse
      2260      (ix) FEATURE:
      2261          (A) NAME/KEY: CDS
      2262          (B) LOCATION: 187..1692
      2264      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
E--> 2266 AAGCGGCGGC AGAAGTTGCC GGCCTGGTGC TCGTAGTGAG GCGCGGAGG
      2267 ACCCGGGACC          60
E--> 2269 TGGGAAGCGG CGGCGGGTTA ACTTCGGCTG AATCACAACC ATTTGGCGCT
      2270 GAGCTATGAC          120
E--> 2272 AAGAGAGCAA ACAAAAAGTT AAAGGAGCAA CCCGGCCATA AGTGAAGAGA
      2273 GAAGTTTATT          180
      2275 GATAAC ATG CTC TTA CGA AGC TCT GGA AAA TTA AAT GTG GGC ACC AAG          228
      2276      Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys
      2277          1          5          10
      2279 AAG GAG GAT GGA GAG AGT ACA GCC CCC ACC CCT CGG CCC AAG ATC CTA          276
      2280 Lys Glu Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu
      2281 15          20          25          30
      2283 CGT TGT AAA TGC CAC CAC CAC TGT CCG GAA GAC TCA GTC AAC AAT ATC          324
      2284 Arg Cys Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile
      2285          35          40          45
      2287 TGC AGC ACA GAT GGG TAC TGC TTC ACG ATG ATA GAA GAA GAT GAC TCT          372
      2288 Cys Ser Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser
      2289          50          55          60
      2291 GGA ATG CCT GTT GTC ACC TCT GGA TGT CTA GGA CTA GAA GGG TCA GAT          420
      2292 Gly Met Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp
      2293          65          70          75
      2295 TTT CAA TGT CGT GAC ACT CCC ATT CCT CAT CAA AGA AGA TCA ATT GAA          468
      2296 Phe Gln Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu
      2297 80          85          90
      2299 TGC TGC ACA GAA AGG AAT GAG TGT AAT AAA GAC CTC CAC CCC ACT CTG          516
      2300 Cys Cys Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu
      2301 95          100          105          110
      2303 CCT CCT CTC AAG GAC AGA GAT TTT GTT GAT GGG CCC ATA CAC CAC AAG          564
      2304 Pro Pro Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys
      2305          115          120          125
      2307 GCC TTG CTT ATC TCT GTG ACT GTC TGT AGT TTA CTC TTG GTC CTC ATT          612
      2308 Ala Leu Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile
      2309          130          135          140
      2311 ATT TTA TTC TGT TAC TTC AGG TAT AAA AGA CAA GAA GCC CGA CCT CGG          660
      2312 Ile Leu Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg
      2313          145          150          155
      2315 TAC AGC ATT GGG CTG GAG CAG GAC GAG ACA TAC ATT CCT CCT GGA GAG          708
      2316 Tyr Ser Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu
      2317          160          165          170
      2319 TCC CTG AGA GAC TTG ATC GAG CAG TCT CAG AGC TCG GGA AGT GGA TCA          756
      2320 Ser Leu Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser

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2321	175				180				185			190					
2323	GGC	CTC	CCT	CTG	CTG	GTC	CAA	AGG	ACA	ATA	GCT	AAG	CAA	ATT	CAG	ATG	804
2324	Gly	Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	
2325					195				200					205			
2327	GTG	AAG	CAG	ATT	GGA	AAA	GGC	CGC	TAT	GGC	GAG	GTG	TGG	ATG	GGA	AAG	852
2328	Val	Lys	Gln	Ile	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	
2329				210					215					220			
2331	TGG	CGT	GGA	GAA	AAG	GTG	GCT	GTG	AAA	GTG	TTC	TTC	ACC	ACG	GAG	GAA	900
2332	Trp	Arg	Gly	Glu	Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	
2333			225					230					235				
2335	GCC	AGC	TGG	TTC	CGA	GAG	ACT	GAG	ATA	TAT	CAG	ACG	GTC	CTG	ATG	CGG	948
2336	Ala	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	
2337		240					245					250					
2339	CAT	GAG	AAT	ATT	CTG	GGG	TTC	ATT	GCT	GCA	GAT	ATC	AAA	GGG	ACT	GGG	996
2340	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	
2341	255				260					265					270		
2343	TCC	TGG	ACT	CAG	TTG	TAC	CTC	ATC	ACA	GAC	TAT	CAT	GAA	AAC	GGC	TCC	1044
2344	Ser	Trp	Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	
2345				275					280					285			
2347	CTT	TAT	GAC	TAT	CTG	AAA	TCC	ACC	ACC	TTA	GAC	GCA	AAG	TCC	ATG	CTG	1092
2348	Leu	Tyr	Asp	Tyr	Leu	Lys	Ser	Thr	Thr	Leu	Asp	Ala	Lys	Ser	Met	Leu	
2349			290					295					300				
2351	AAG	CTA	GCC	TAC	TCC	TCT	GTC	AGC	GGC	CTA	TGC	CAT	TTA	CAC	ACG	GAA	1140
2352	Lys	Leu	Ala	Tyr	Ser	Ser	Val	Ser	Gly	Leu	Cys	His	Leu	His	Thr	Glu	
2353		305					310					315					
2355	ATC	TTT	AGC	ACT	CAA	GGC	AAG	CCA	GCA	ATC	GCC	CAT	CGA	GAC	TTG	AAA	1188
2356	Ile	Phe	Ser	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	
2357		320					325					330					
2359	AGT	AAA	AAC	ATC	CTG	GTG	AAG	AAA	AAT	GGA	ACT	TGC	TGC	ATA	GCA	GAC	1236
2360	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	Cys	Ile	Ala	Asp	
2361	335				340					345				350			
2363	CTG	GGC	TTG	GCT	GTC	AAG	TTC	ATT	AGT	GAC	ACA	AAT	GAG	GTT	GAC	ATC	1284
2364	Leu	Gly	Leu	Ala	Val	Lys	Phe	Ile	Ser	Asp	Thr	Asn	Glu	Val	Asp	Ile	
2365				355					360					365			
2367	CCA	CCC	AAC	ACC	CGG	GTT	GGC	ACC	AAG	CGC	TAT	ATG	CCT	CCA	GAA	GTG	1332
2368	Pro	Pro	Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Pro	Pro	Glu	Val	
2369			370					375					380				
2371	CTG	GAC	GAG	AGC	TTG	AAT	AGA	AAC	CAT	TTC	CAG	TCC	TAC	ATT	ATG	GCT	1380
2372	Leu	Asp	Glu	Ser	Leu	Asn	Arg	Asn	His	Phe	Gln	Ser	Tyr	Ile	Met	Ala	
2373		385					390					395					
2375	GAC	ATG	TAC	AGC	TTT	GGA	CTC	ATC	CTC	TGG	GAG	ATT	GCA	AGG	AGA	TGT	1428
2376	Asp	Met	Tyr	Ser	Phe	Gly	Leu	Ile	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Cys	
2377		400				405				410							
2379	GTT	TCT	GGA	GGT	ATA	GTG	GAA	GAA	TAC	CAG	CTT	CCC	TAT	CAC	GAC	CTG	1476
2380	Val	Ser	Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	His	Asp	Leu	
2381	415				420					425				430			
2383	GTG	CCC	AGT	GAC	CCT	TCT	GAG	GAC	ATG	AGA	GAA	ATT	GTG	TGC	ATG		1524
2384	Val	Pro	Ser	Asp	Pro	Ser	Tyr	Glu	Asp	Met	Arg	Glu	Ile	Val	Cys	Met	
2385				435				440						445			

RAW SEQUENCE LISTING

DATE: 10/15/2001

PATENT APPLICATION: US/09/039,177D

TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt

Output Set: N:\CRF3\10152001\I039177D.raw

```

2387 AAG AAG TTA CGG CCT TCA TTC CCC AAT CGA TGG AGC AGT GAT GAG TGT      1572
2388 Lys Lys Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys
2389           450           455           460
2391 CTC AGG CAG ATG GGG AAG CTT ATG ACA GAG TGC TGG GCG CAG AAT CCT      1620
2392 Leu Arg Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro
2393           465           470           475
2395 GCC TCC AGG CTG ACG GCC CTG AGA GTT AAG AAA ACC CTT GCC AAA ATG      1668
2396 Ala Ser Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met
2397           480           485           490
E--> 2399 TCA GAG TCC CAG GAC ATT AAA CTC TGACGTCAGA TACTTGTGGA CAGAGCAAGA
W--> 2400      1722
      2401 Ser Glu Ser Gln Asp Ile Lys Leu
W--> 2402 495           500
E--> 2404 ATTTACACAGA AGCATCGTTA GCCCAAGCCT TGAACGTTAG CCTACTGCCC
      2405 AGTGAGTTCA      1782
E--> 2407 GACTTTCCTG GAAGAGAGCA CGGTGGGCAG ACACAGAGGA ACCCAGAAAC
      2408 ACGGATTCAT      1842
E--> 2410 CATGGCTTTC TGAGGAGGAG AAACGTGTTG GGTAACCTGT TCAAGATATG
      2411 ATGCATGTTG      1902
      2413 CTTTCTAAGA AAGCCCTGTA TTTTGAATTA CCATTTTTTTT ATAAAAAAAAA      1952
2752 (2) INFORMATION FOR SEQ ID NO: 32:
2753     (i) SEQUENCE CHARACTERISTICS:
2754         (A) LENGTH: 175 amino acids
2755         (B) TYPE: amino acid
2756         (D) TOPOLOGY: linear
2758     (ii) MOLECULE TYPE: peptide
2760     (vi) ORIGINAL SOURCE:
2761         (A) ORGANISM: Mouse
2763     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:
2765 Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala
2766           5           10           15
2767 Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln Asp
2768           20           25           30
2769 Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly Met
2770           35           40           45
2771 Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly Thr
2772           50           55           60
2773 Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys Gly
2774           65           70           75           80
2775 Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu Leu
2776           85           90           95
2777 Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His Glu
2778           100          105          110
2779 Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His Arg
2780           115          120          125
2781 Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala Cys
2782           130          135          140
2783 Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser Ala
2784           145          150          155          160

```

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Input Set : A:\Lud-5539 sequence listing.txt

Output Set: N:\CRF3\10152001\I039177D:raw

2785 Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
E--> 2786

165 170

2909 (2) INFORMATION FOR SEQ ID NO: 35:
2910 (i) SEQUENCE CHARACTERISTICS:
2911 (A) LENGTH: 536 amino acids
2912 (B) TYPE: amino acid
2913 (D) TOPOLOGY: linear
2915 (ii) MOLECULE TYPE: peptide
2917 (vi) ORIGINAL SOURCE:
2918 (A) ORGANISM: MOUSE
2920 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

2923	Met	Thr	Ala	Pro	Trp	Ala	Ala	Leu	Ala	Leu	Leu	Trp	Gly	Ser	Leu	Cys
2924					5					10					15	
2926	Ala	Gly	Ser	Gly	Arg	Gly	Glu	Ala	Glu	Thr	Arg	Glu	Cys	Ile	Tyr	Tyr
2927				20					25					30		
2928	Asn	Ala	Asn	Trp	Glu	Leu	Glu	Arg	Thr	Asn	Gln	Ser	Gly	Leu	Glu	Arg
2929				35				40					45			
2930	Cys	Glu	Gly	Glu	Gln	Asp	Lys	Arg	Leu	His	Cys	Tyr	Ala	Ser	Trp	Arg
2931		50					55					60				
2932	Asn	Ser	Ser	Gly	Thr	Ile	Glu	Leu	Val	Lys	Lys	Gly	Cys	Trp	Leu	Asp
2933	65					70				75					80	
2934	Asp	Phe	Asn	Cys	Tyr	Asp	Arg	Gln	Glu	Cys	Val	Ala	Thr	Glu	Glu	Asn
2935				85						90					95	
2936	Pro	Gln	Val	Tyr	Phe	Cys	Cys	Cys	Glu	Gly	Asn	Phe	Cys	Asn	Glu	Arg
2937				100					105					110		
2938	Phe	Thr	His	Leu	Pro	Glu	Pro	Gly	Pro	Glu	Val	Thr	Tyr	Glu	Pro	
2939			115					120				125				
2940	Pro	Pro	Thr	Ala	Pro	Thr	Leu	Leu	Thr	Val	Leu	Ala	Tyr	Ser	Leu	Leu
2941			130				135					140				
2942	Pro	Ile	Gly	Gly	Leu	Ser	Leu	Ile	Val	Leu	Leu	Ala	Phe	Trp	Met	Tyr
2943	145					150					155				160	
2944	Arg	His	Arg	Lys	Pro	Pro	Tyr	Gly	His	Val	Asp	Ile	His	Glu	Val	Arg
2945				165						170					175	
2946	Gln	Cys	Gln	Arg	Trp	Ala	Gly	Arg	Arg	Asp	Gly	Cys	Ala	Asp	Ser	Phe
2947				180				185						190		
2948	Lys	Pro	Leu	Pro	Phe	Gln	Asp	Pro	Gly	Pro	Pro	Pro	Pro	Ser	Pro	Leu
2949				195				200					205			
2950	Val	Gly	Leu	Lys	Pro	Leu	Gln	Leu	Leu	Glu	Ile	Lys	Ala	Arg	Gly	Arg
2951			210				215					220				
2952	Phe	Gly	Cys	Val	Trp	Lys	Ala	Gln	Leu	Met	Asn	Asp	Phe	Val	Ala	Val
2953	225					230					235				240	
2954	Lys	Ile	Phe	Pro	Leu	Gln	Asp	Lys	Gln	Ser	Trp	Gln	Ser	Glu	Arg	Glu
2955				245						250					255	
2956	Ile	Phe	Ser	Thr	Pro	Gly	Met	Lys	His	Glu	Asn	Leu	Leu	Gln	Phe	Ile
2957				260					265					270		
2958	Ala	Ala	Glu	Lys	Arg	Gly	Ser	Asn	Leu	Glu	Val	Glu	Leu	Trp	Leu	Ile
2959			275					280					285			
2960	Thr	Ala	Phe	His	Asp	Lys	Gly	Ser	Leu	Thr	Asp	Tyr	Leu	Lys	Gly	Asn
2961		290					295					300				

RAW SEQUENCE LISTING

DATE: 10/15/2001

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TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt

Output Set: N:\CRF3\10152001\I039177D.raw

```

2962 Ile Ile Thr Trp Asn Glu Leu Cys His Val Ala Glu Thr Met Ser Arg
2963 305 310 315 320
2964 Gly Leu Ser Tyr Leu His Glu Asp Val Pro Trp Cys Arg Gly Glu Gly
2965 325 330 335
2966 His Lys Pro Ser Ile Ala His Arg Asp Phe Lys Ser Lys Asn Val Leu
2967 340 345 350
2968 Leu Lys Ser Asp Leu Thr Ala Val Leu Ala Asp Phe Gly Leu Ala Val
2969 355 360 365
2970 Arg Phe Glu Pro Gly Lys Pro Pro Gly Asp Thr His Gly Gln Val Gly
2971 370 375 380
2972 Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe
2973 385 390 395 400
2974 Gln Arg Asp Ala Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val
2975 405 410 415
2976 Leu Trp Glu Leu Val Ser Arg Cys Lys Ala Ala Asp Gly Pro Val Asp
2977 420 425 430
2978 Glu Tyr Met Leu Pro Phe Glu Glu Glu Ile Gly Gln His Pro Ser Leu
2979 435 440 445
2980 Glu Glu Leu Gln Glu Val Val Val His Lys Lys Met Arg Pro Thr Ile
2981 450 455 460
2982 Lys Asp His Trp Leu Lys His Pro Gly Leu Ala Gln Leu Cys Val Thr
2983 465 470 475 480
2984 Ile Glu Glu Cys Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly
2985 485 490 495
2986 Cys Val Glu Glu Arg Val Ser Leu Ile Arg Arg Ser Val Asn Gly Thr
2987 500 505 510
2988 Thr Ser Asp Cys Leu Val Ser Leu Val Thr Ser Val Thr Asn Val Asp
E--> 2989 515 520 525
2990 Leu Leu Pro Lys Glu Ser Ser Ile
E--> 2991 530 535
3081 (2) INFORMATION FOR SEQ ID NO: 37:
3082 (i) SEQUENCE CHARACTERISTICS:
3083 (A) LENGTH: 97 amino acids
3084 (B) TYPE: amino acid
3085 (D) TOPOLOGY: linear
3087 (ii) MOLECULE TYPE: peptide
3089 (vi) ORIGINAL SOURCE:
3090 (A) ORGANISM: C. elegans
3092 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:
3095 Cys His Cys Ser Arg Glu Val Gly Cys Asn Ala Arg Thr Thr Gly Trp
E--> 3096 5 10 15
3097 Val Pro Gly Ile Glu Phe Leu Asn Glu Thr Asp Arg Ser Phe Tyr Glu
E--> 3098 20 25 30
3099 Asn Thr Cys Tyr Thr Asp Gly Ser Cys Tyr Gln Ser Ala Arg Pro Ser
E--> 3100 35 40 45
3101 Pro Glu Ile Ser His Phe Gly Cys Met Asp Glu Lys Ser Val Thr Asp
E--> 3102 50 55 60
3103 Glu Thr Glu Phe His Asp Thr Ala Ala Lys Val Cys Thr Asn Asn Thr
E--> 3104 65 70 75 80

```

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Input Set : A:\Lud-5539 sequence listing.txt

Output Set: N:\CRF3\10152001\I039177D.raw

```

3105 Lys Asp Pro His Ala Thr Val Trp Ile Cys Cys Asp Lys Gly Asn Phe
E--> 3106                85                90                95
3107 Cys
3111 (2) INFORMATION FOR SEQ ID NO: 38:
3112     (i) SEQUENCE CHARACTERISTICS:
3113         (A) LENGTH: 6 amino acids
3114         (B) TYPE: amino acid
3115         (D) TOPOLOGY: linear
3117     (ii) MOLECULE TYPE: peptide
3119     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
3121 Asp Leu Lys Pro Glu Asn
E--> 3122                5
3128 (2) INFORMATION FOR SEQ ID NO: 39:
3129     (i) SEQUENCE CHARACTERISTICS:
3130         (A) LENGTH: 6 amino acids
3131         (B) TYPE: amino acid
3132         (D) TOPOLOGY: linear
3134     (ii) MOLECULE TYPE: peptide
3136     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
3138 Asp Leu Ala Ala Arg Asn
E--> 3139                5
3142 (2) INFORMATION FOR SEQ ID NO: 40:
3143     (i) SEQUENCE CHARACTERISTICS:
3144         (A) LENGTH: 6 amino acids
3145         (B) TYPE: amino acid
3146         (D) TOPOLOGY: linear
3148     (ii) MOLECULE TYPE: peptide
3150     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:
3152 Asp Ile Lys Ser Lys Asn
E--> 3153                5
3156 (2) INFORMATION FOR SEQ ID NO: 41:
3157     (i) SEQUENCE CHARACTERISTICS:
3158         (A) LENGTH: 6 amino acids
3159         (B) TYPE: amino acid
3160         (D) TOPOLOGY: linear
3162     (ii) MOLECULE TYPE: peptide
3164     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:
3166 Asp Phe Lys Ser Lys Asn
E--> 3167                5
3170 (2) INFORMATION FOR SEQ ID NO: 42:
3171     (i) SEQUENCE CHARACTERISTICS:
3172         (A) LENGTH: 6 amino acids
3173         (B) TYPE: amino acid
3174         (D) TOPOLOGY: linear
3176     (ii) MOLECULE TYPE: peptide
3178     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:
3180 Asp Leu Lys Ser Ser Asn
E--> 3181                5
3184 (2) INFORMATION FOR SEQ ID NO: 43:

```

RAW SEQUENCE LISTING

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TIME: 13:47:04

Input Set : A:\Lud-5539 sequence listing.txt

Output Set: N:\CRF3\10152001\I039177D.raw

```

3185      (i) SEQUENCE CHARACTERISTICS:
3186          (A) LENGTH: 6 amino acids
3187          (B) TYPE: amino acid
3188          (D) TOPOLOGY: linear
3190      (ii) MOLECULE TYPE: peptide
3192      (ix) FEATURE:
3193          (D) OTHER INFORMATION: First Xaa is Thr or Ser;
3194 fourth Xaa is Tyr or Phe; Each other Xaa
3195 may be any amino acid
3197      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
W--> 3199 Gly Xaa Xaa Xaa Xaa Xaa
E--> 3200      5
3203 (2) INFORMATION FOR SEQ ID NO: 44:
3204      (i) SEQUENCE CHARACTERISTICS:
3205          (A) LENGTH: 6 amino acids
3206          (B) TYPE: amino acid
3207          (D) TOPOLOGY: linear
3209      (ii) MOLECULE TYPE: peptide
3211      (ix) FEATURE:
3212          (D) OTHER INFORMATION: Fisrt Xaa is any amino acid;
3213 second Xaa is Ile or Val;
3214 third Xaa is Lys or Arg;
3215 fourth Xaa is Thr or Met.
3217      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:
W--> 3219 Xaa Pro Xaa Xaa Trp Xaa
E--> 3220      5
3223 (2) INFORMATION FOR SEQ ID NO: 45:
3224      (i) SEQUENCE CHARACTERISTICS:
3225          (A) LENGTH: 6 amino acids
3226          (B) TYPE: amino acid
3227          (D) TOPOLOGY: linear
3229      (ii) MOLECULE TYPE: peptide
3231      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:
3233 Gly Thr Arg Arg Tyr Met
E--> 3234      5
3236 (2) INFORMATION FOR SEQ ID NO: 46:
3237      (i) SEQUENCE CHARACTERISTICS:
3238          (A) LENGTH: 6 amino acids
3239          (B) TYPE: amino acid
3240          (D) TOPOLOGY: linear
3242      (ii) MOLECULE TYPE: peptide
3244      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
3246 Gly Thr Ala Arg Tyr Met
E--> 3247      5

```

VERIFICATION SUMMARY

DATE: 10/15/2001

PATENT APPLICATION: US/09/039,177D

TIME: 13:47:05

Input Set : A:\Lud-5539 sequence listing.txt

Output Set: N:\CRF3\10152001\I039177D.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:85 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:98 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:1
M:254 Repeated in SeqNo=1
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:207 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:209 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:233 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:236 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:238 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:340 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:353 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:3
M:254 Repeated in SeqNo=3
L:357 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:442 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:444 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:448 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:452 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:456 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:460 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:464 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:468 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:472 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:476 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:480 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:484 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:488 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:542 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:632 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:645 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:5
M:254 Repeated in SeqNo=5
L:721 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:723 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:727 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:731 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:735 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:739 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:743 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:747 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:751 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:755 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:759 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5

VERIFICATION SUMMARY

DATE: 10/15/2001

PATENT APPLICATION: US/09/039,177D

TIME: 13:47:05

Input Set : A:\Lud-5539 sequence listing.txt

Output Set: N:\CRF3\10152001\I039177D.raw

L:763 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:767 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:771 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:775 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:779 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:783 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:787 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:791 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:794 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:796 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:940 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1080 M:254 E: No. of Bases conflict, Input:0 Counted:1585 SEQ:7
M:254 Repeated in SeqNo=7
L:1210 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1223 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:9
M:254 Repeated in SeqNo=9
L:1227 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1389 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1479 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1492 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:11
M:254 Repeated in SeqNo=11
L:1727 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1740 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:13
M:254 Repeated in SeqNo=13
L:1750 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1992 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2133 M:254 E: No. of Bases conflict, Input:0 Counted:1584 SEQ:15
M:254 Repeated in SeqNo=15
L:2253 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2266 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:17
M:254 Repeated in SeqNo=17
L:2503 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2521 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2539 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2557 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2575 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2593 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2611 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:2786 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32
L:2989 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
M:332 Repeated in SeqNo=35
L:3096 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:37
M:332 Repeated in SeqNo=37
L:3122 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
L:3139 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39
L:3153 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:40
L:3167 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:41
L:3181 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42

VERIFICATION SUMMARY

DATE: 10/15/2001

PATENT APPLICATION: US/09/039,177D

TIME: 13:47:05

Input Set : A:\Lud-5539 sequence listing.txt

Output Set: N:\CRF3\10152001\I039177D.raw

L:3199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:3200 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:43
L:3219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:3220 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:44
L:3234 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
L:3247 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ ~~An initial~~ or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

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NOV 13 2001

Raw Sequence Listing Error Summary

TECH CENTER 1600/2900

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/039177D

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

- 1 ☒ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped.

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence.
- 11 ☐ **Use of <220>** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n** n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MII - Biotechnology Systems Branch - 08/21/2001

Error Summary Sheet
See Error Summary Supplement